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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| | 7 | | Abg66915 Streptoco | Str | Abu01234 S. pneumo | | | | Abp25843 Streptoco | Adk68537 Mycoplasm | Adk68536 Mycoplasm | Aaw22727 Membrane | Ф | | Abp71709 M161 anti | Aay05332 Inflammat | Aap93343 Gene enco | | Aao15867 Mycoplasm | | Aau01860 Mycoplasm | Aao15862 Mutant My | Aao15861 Mycoplasm | соріав | Description | |

New apoprotein antigens encoded by mhp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing diseases

King KW,

Madura RA,

Rosey EL;

(PFIZ) PFIZER PROD INC.

29-SEP-1999;

99US-0156602P

N-PSDB; AAS03285. WPI; 2001-309781/33.

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| ADH88120 | ABU13546 | ABU88295 | ABP43267 | AAY00048 | ABII 3547 | ABU88296 | ABP43268 | AAY00049 | ADB09398 | ABG66913 | ABP29943 | ABP25842 | ABP29678 | ABP30886 | ADH88119 | ADC95457 | ADC45089 | ABP54560 | AAW55066 |
| 24522 | Abu13546 | Abu88295 | Abp43267 | Aav00048 | Abu13547 | Abu88296 | Abp43268 | Aay00049 | Adb09398 | Abg66913 | Abp29943 | Abp25842 | Abp29678 | Abp30886 | Adh88119 | Adc95457 | Adc45089 | Abp54560 | Aaw55066 |
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RESULT 1 AAUOL859 ID OALO XX AAUO XX AAUO XX AY AC AAUO XX MYCO XX MYCO XX MHP3 XX IMMU XX IMMU XX MHS3 KW IMMU XX MHS6 FT Misc FT Mis /note= "Encoded by TGA" Misc-difference 152 Misc-difference Misc-difference 198 Misc-difference Misc-difference 138 Misc-difference 99 Mycoplasma hyopneumoniae. MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; antibody; immunoassay; immunotherapy; anti-idiotypic antibody. Mycoplasma hyopneumoniae MHP3 antigen. 07-SEP-2001 AAU01859; AAU01859 standard; protein; 451 26-SEP-2000; 2000EP-00308421. 11-APR-2001. EP1090995-A2 Misc-difference (first entry) Location/Qualifiers /note= "Encoded by TGA" note= "Encoded by TGA"

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Best Local
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                                                                                                                                                   16-JAN-2003
                                                                                                                                                                                                           AAO15861 standard; protein;
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Matches 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae in animals, especially pigs.
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Query Match 92.8%;
Best Local Similarity 99.8%;
Matches 419; Conservative
                                                                                                                                                  The invention comprises the amino acid and coding sequences of Mycoplasma hyopneumoniae mhp3 proteins, the invention also comprises novel apoprotein antigens encoded by the M. hyopneumoniae mhp3 gene. M. hyopneumoniae is a bacterial pathogen that causes enzoctic mycoplasmal pneumoniae in pigs. The mhp3 genes, proteins and apoprotein antigens of the invention are useful in the manufacture of a vaccine for treating/ preventing a disease or disorder caused by infection with M. hyopneumoniae in an animal, especially a pig. The present amino acid sequence represents a mutant version of the Mycoplasma hyopneumoniae mhp3 protein which was modified for expression in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae in animals, especially pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              King
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 20-21; 38pp; English.
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                                                                                                      Sequence
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hyopneumoniae infection.
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Score 2134; DB 5;
Pred. No. 3.4e-152;
0; Mismatches 1;
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                                         New apoprotein antigens encoded by mhp3 hyopneumoniae useful as a vaccine for to caused by Mycoplasma hyopneumoniae.
                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                            MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; mutant; antibody; immunoassay; immunotherapy; anti-idiotypic antibody; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001
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N-PSDB; AAS03286.
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                      Claim 4; Page 19-21; 38pp; English
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                                                                                                                                                                                                                                                                  /note= "Encoded by AATTACCGATAT"
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treating or preventing
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The sequence represents Mycoplasma hyopneumoniae a recombinant MHP3

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ARRESULT 5
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ID AAR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
07-MAR-1994
                             Misc-difference
                                                                                                            Misc-difference
                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                 Mycoplasma hyorhinis
                                                                                                                                                                                                                                                                                                                 anti-idiotypic
                                                                                                                                                                                                                                                                                                                                       Regression associated antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR40856 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR40856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 423
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                                                                                                                                                                                                                                                                                                                                                                                             regression associated antigen
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                                                                                                                                                                                                                                                                                                                    antibodies;
                                                                                                                                                                                  Location/Qualifiers
                                                      /note= "Tryptophan
hyorhinis."
                                                                                                                                 hyorhinis
                                                                                                                                                       note= "Tryptophan
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Pred. No. 2.6e-150;
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tumour regression.
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Best Local
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16-SEP-1987;
11-DEC-1987;
04-JAN-1988;
16-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regression associated antigens (RAA's) are identified in material from neoplastic cells by their immunological reactivity with regression associated antibodies from the serum of patients diagnosed as undergoing regression of a tumour. RAA's can be used for tumour immunotherapy and for producing and purifying antibodies which can be used for tumour diagnosis, localisation and therapy. The antibodies can also be used for the production of anti-idiotypic antibodies which can also be used in immunotherapy. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a regression-associated antigen from M. hyorhinis - is used to obtain prods. for diagnosis, localisation and therapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ47816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy. (Updated on 25-MAR-2003 to correct
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                                                                                                            300
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                               VIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGY
                                                                                                                                                                                                                                                                               SSLANTNKNVWVLSGFQHGDAFTRWLKIPEN----KQLFTEKNIIILGIDW---TDTEN
                                                                                                                                                                                                                                                                                                                                         NKHFGLNMAIVTAGGTVNDNSFNOSSWEAI----QQLGALTG-GEITSVDSSTABLEGKY 127
                                                                                                                                                                                                                                                                                                                                                                                             GLVFPLSAIAT-ISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 AA;
TIPAEEVRKTLEIPEM--PDKQPDKQQESLDKLITDIN
                         SKFLGSFRSFKLTNPANATVYKGISDDFVGVSNSTVADADKVKAQEFLNEATADFKKQIQ
                                                                                SSVVDAIKKSNKDTKYLIGVDTDQSKIFPPA-TVFFTSIEKHLGRTIYEVLTDIWLKKED
                                                                                                    EIFSDII--ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSN
                                                                                                                                                                 LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLT
                                                                                                                                                                                                                                                       KNFLNGNKNVWILTGFQQGQEFPKFLKQTDSNGKKYSDLLAEKKVIIVAVDWDLSKEDKD
                                                                                                                                                                                                                                                                                                                                                                       GTISTVASVATFVSCG----ETDKEGKII-----RIFD----NSFVKDRQAEIEKA----
                                            SRNLAGFEFGK----KSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTK 413
                                                                                                                                        LAGIAKYNNDNPTAKVTISDNNINIDTGF-ISNDKTATFINGIVNKS--SLVLPVVGSLT
                                                                                                                                                                                                                                                                                                              -KNFDENTYLLTAGGTYQDKSENQSIWEAVLEHYDQIEKTTNLDRVSQETNQSELIGKY
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87US-00097910.
87US-00131815.
88US-00138923.
90US-00474730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghosh-Dastidar
                                                                                                                                                                                                                                                                                                                                                                                                                                           31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 714.5; DB 2
Pred. No. 3.5e-45;
8; Mismatches 150
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Best Local Similarity
Matches 173; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises the amino acid and coding sequences of Mycoplasma hyopneumoniae mhp3 proteins, the invention also comprises novel apoprotein antigens encoded by the M. hyopneumoniae mhp3 gene. M. hyopneumoniae is a bacterial pathogen that causes enzottic mycoplasmal pneumonia in pigs. The mhp3 genes, proteins and apoprotein antigens of the invention are useful in the manufacture of a vaccine for treating/ preventing a disease or disorder caused by infection with M. hyopneumoniae in an animal, especially a pig. The present amino acid sequence represents the Mycoplasma hyorhinis Ag234-5 protein which is shown in a figure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 457 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use vaccines to prevent and treat diseases caused by infection with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO15867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma hyopneumoniae in animals, especially pigs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma hyorhinis Ag234-5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO15867 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PFIZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoprotein antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KW, Madura RA,
   240
                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
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   LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLT 299
                                                                                                                                                                                                                                                                                SSLANTNKNVWVLSGFQHGDAFTRWLKIPEN----KQLFTEKNIIILGIDW----TDTEN 179
                                                                                                                                                                                                                                                                                                                                                                                                                         NKHFGLNMAIVTAGGTVNDNSFNQSSWEAI----QQLGALTG-GEITSVDSSTAELEGKY 127
                                                                         LIKAGHFISLLYKTEEAGFIAGYASSKFLAYKFPNDEAKRTIAPFGGGHGAGVTDFIAGF
                                                                                                                                    VIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGY 239
                                                                                                                                                                                                                  KNFLNGNKNVWILTGFQQGQEFPKFLKQTDSNGKKYSDLLAEKKVIIVAVDWDLSKEDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTISTVASVATFVSCG----ETDKEGKII-----RIFD----NSFVKDRQAEIEKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLVFPLSAIAT-ISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADA
                                                                                                                                                                                                                                                                                                                                                          - KNFDFNTVLLTAGGTVQDKSFNQSIWEAVLEHYDQIEKTTNLDRVSQETNNQSELIGKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.7%; Score 706; DB 5; Length 45
38.4%; Pred. No. 1.5e-44;
tive 87; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosey EL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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ETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN 92

Indels

41;

Gaps

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RESULT 7
AAR67522
ID AAR66
XX AAR66
XX CANC
DT 06-0
DT 06-0
DT CANC
DX CANC
XX CANC
XX CANC
XX CANC
XX HOMO
XX HOMO
XX HOMO
XX HOMO
XX HOMO
PT Misc
FT Misc
FT
Query Match
Best Local Similarity
Matches 168; Conserv
                                                                                                                                                                    AAQ79124 encodes AAR67582 a protein involved in cancer metastasis, we may be used for the study of metastaic mechanisms, and for clinical to determine the presence or absence of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-040317/06.
N-PSDB; AAQ79124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-1995
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                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                             Claim 1; Page 2; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                    DNA encoding polypeptide involved in study of the mechanism of metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP06319559-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer metastasis; clinical tests; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer metastasis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
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                                                                                                                   432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANPT-NYKSVLGIPTMLINDNDAKDNEKASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRNLAGFEFGK----KSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSVVDAIKKSNKDTKYLIGVDTDQSKIFSPA-TVFFTSIEKHLGRTIYQVLTDIWLKKED 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIFSDII--ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKFLGSFRSFKLTNPANATVYKGISDDFVGVSNSTVADADKVKAQEFLNEATADFKKQIQ 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-00144165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93JP-00144165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "corresponding codon TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "corresponding codon TGA"
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                           30.2%;
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Score 694.5; DB 2;
Pred. No. 1.1e-43;
1; Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                    cancer metastasis - useful and in clinical tests.
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                                                   DB 2;
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                                                      Length
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RESULT 8
AAP93343
ID AAP9
AC AAP9
XX AAP9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding the 43 kd regression-associated Mycoplasma hyorhinis.
Tumour regression-associated antigens and antibodies - used in diagnostic tests, monitoring course of therapy and for therapy in cancer patients.
                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                 16-SEP-1987;
11-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour regression-associated antigens (RA Ag); therapy monitoring; cancer therapy; Mycoplasma
                                                                     WPI; 1989-087638/12.
N-PSDB; AAN90684.
                                                                                                                                                                                      (ITGE-) INT GENETIC ENG INC (INGE-) INGENE INT GENETIC. (INGE-) INGENE INT GENETIC.
                                                                                                                                                                                                                                                                                                                                                    16-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                             EP308265-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma
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01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP93343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP93343 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFNOSSWEAI----OQLGALTG-GEITSVDSSTAELEGKYSSLANTNKNVWVLSGFOHGD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNINIDTGF-ISNDKTATFINGIVNKS--SLVLPVAGSLTSSVVDAIKKSNKDTKYLIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFPKFLKQTDSNGKKYSDLLAEKKVIIVAVDWDLSKEDKDLIKAGHFISLLYKTEEAGFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKOPDKOOESL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGYANAS FLAKKF PSD PTKRSAIVIGGGIS PAVTD FIAGYLAGIKAWNLKNSDKKTKITT
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Matches 171; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    Inflammatory
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N-PSDB; AAX33847.
                           Misc-difference
                                                                                                                                                                                    Mycoplasma
                                                                                                                                                                                                                                                                  M161; antigen; cytotoxic T-lymhpocyte inducer; CTL;
                                                                                                                                                                                                                                                                                                                    M161 antigen
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                                                                                                            Location/Qualifiers
/note= "Encoded by TGA; unexplained stop
                                                                             note= "Encoded by TGA; unexplained
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to cytotoxic T-lymhpocyte (CTL)-inducers containing the M161 antigen, its partial peptide or their salt. The activity of CTL-inducers of the invention may be described as cytostatic. The antigen or its peptide fragment are applicable in anticancer agents for the prevention or treatment of cancer. The antigen and its derivative have superior CTL-inductive effect, giving anticancer agents that have low toxicity. The current sequence represents the M161 antigen amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M161 antigen, its peptide fragment or their salt with e.g. inductive effect, applicable in anticancer agents combined antigen for preventing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 94pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2001; 2001JP-00182250
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DB; ABZ59715.
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                                                                                   LYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINVVLSSTPADVKYNPHVIL
                                                                                                                          --FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTENEGFAKGI
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                               SVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                                                  ESAYNSALSAGHKIWYLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW 163
                                                                                                                                                                                                          EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIILGIDWTDTENVIPT 183
                                                                                                                                                                                                                                    VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKOTGIEINNVEPS-SNF 106
                                                                                                                                                                                                                                                           EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
                                                                                                                                                                                                                                                                                       MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTINANGKO
                                                          AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-
                                                                                                            KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-----KDKPSTLL
                                                                                                                                                                                                                                                                                                                                    17.2%; Score 394.5; DB 6; ilarity 26.8%; Pred. No. 4.2e-21; Conservative 101; Mismatches 174;
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           -YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides novel immunoregulatory factor designated IL-X which has been isolated Mycoplasma and polumuclectides encoding such polypeptides. The polynuclectide is useful for augmenting proliferation of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 9; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide, useful for augmenting proliferation {\tt T} lymphocytes.
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(BLAZ/) BLAZAR B A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma
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                                                                                                                                                           VVKNAEL----LKLKPILITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF 106
                                                                                                                                                                                            EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
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GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 428;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of B
                                                      163
                                                                                                                                                                                                                                                                   52
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RESULT 12
ADK68538
ID ADK68538
XX ADK68
XX ADK68
XX ADK68
XX IMMUN
XX IME
PT Pepti
PT 29-OC
XX IME
PA (MEBE
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P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
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                                                     The invention provides novel immunoregulatory factor designated IL-X which has been isolated Mycoplasma and polunucleotides encoding such polypeptides. The polynucleotide is useful for augmenting proliferation of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-X precursor protein.
                                                                                                                                                                                                                                                                          New isolated polynucleotide, useful for augmenting proliferation T lymphocytes.
                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-401108/38.
N-PSDB; ADK68535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK68538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK68538 standard;
     Sequence
                                                                                                                                                                                                                       Claim 26; SEQ ID NO 16; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma fermentans IL-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                              Webb AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6506892-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoregulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WEBB/) WEBB A C.
(BLAZ/) BLAZAR B A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-----KDKPSTLL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- FYSLQENIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGI
     428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEKEEGYKPYVVKDKKADKKWSHFGTQ------KEKWIGVAENHFSNTEEQAKINNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYYNOKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                              Blazar BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fermentans.
     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0063701P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00182625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Signal_peptide 25. .428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Mature IL-X protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation.
                                                                                                                                                                                                                                                                                                            of B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
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```

Matches 126; Query Match

Conservative

100;

Mismatches

Indels Length

Gaps

20;

17.0%; 26.8%;

Score 390.5; DB 7 Pred. No. 8.4e-21;

7;

428; 69;

Local Similarity

B. Charles Barbers

```
RESULT 13
AAW22777
ID AAW22
XX AAW22
XX AAW22
XX AAW22
XX AAW22
XX MA61P
XX MA61P
XX MOdif
FT MODIF
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ર્
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                                                                                                                                                                                                                                                                                                                                 JP09157295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M161Ag; membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane protein M161Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22727
Membrane protein M161Ag - useful in development of leukaemia treating
                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                          WPI; 1997-369470/34.
                                                                                                                                                                            05-DEC-1995;
                                                                                                                                                                                                                            05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 -- FYSLQFNIKESAFTTGYAIASWLSEQ--- DESKRVVASFGGGAFFGVTTFNEGFAKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 LEKEEGYKPYVVKDKKADKKWSHFGTQ-----KEKWIGVAENHFSNTEEQAKINNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                            KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVAGPAT -- FETVRLANKGQYVIGVDSDQGMI -- QDKDRILTSVLKHIKQAVYETLLDLI 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-----KDKPSTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVKNAEL-----LKLKPILITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEAIKMEKE----LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTTNANGKO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                            GIJUTSU
                                                                                                                                                                               95JP-00344504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
163
                                                                                                                                                                                                                                                                                                                                                                                                                                                              348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "selenocysteine"
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "selenocysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "selenocysteine"
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a membrane protein designated M161Ag. Oligonucleotide probes for the cDNA were designed from putative N-terminal M161Ag peptide sequences isolated from P19 cells. M161Ag can be used in the development of a leukaemia treating agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 429 AA;
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                                                                                                                                                                                                                                                             06-MAY-2004
                                                                                                                                                                      Mycoplasma fermentans
                                                                                                                                                                                                                                                                                                                     ADK68536 standard;
                                                        29-OCT-1997;
                                                                                 29-OCT-1998;
                                                                                                                14-JAN-2003
                                                                                                                                           US6506892-B1
                                                                                                                                                                                                  Immunoregulatory factor; IL-X; lymphocyte proliferation.
                                                                                                                                                                                                                              Mycoplasma fermentans IL-X mature
             (WEBB/) WEBB A C.
(BLAZ/) BLAZAR B A.
                                                                                                                                                                                                                                                                                                                                                                                                                         398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 -SNFESAYNSALSAGHKIXVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIET 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 NGKOVVKNAEL-----LKLKPVLITDEGKIDDKSFNOSAFEALKAINKOTGIEINNVEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQIT----DVSKISGLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAGIKAMNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS------KDKP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYKX--FYSLOFNIKESAFTTGYALASXLSEQ---DESKRVVASFGGGAFPGVTTFNEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIPTGRYINLTYKTEBAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-A 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVILSVAGPAT -- FETVTLPNKGQYVIGVDSDQGMI -- QDKDRILTSVLKHIKQAVYETL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLLAVAGPLITEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKGIPYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAELEGKYSSLANTNKNVWVLSGFOHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTEN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
                                                                                                                                                                                                                                                                                                                                                                                                                      TEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
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                                                                                                                                                                                                                                                           (first entry)
                                                        97US-0063701P
                                                                                   98US-00182625
                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Mismatches 174;
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RESULT 15
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Best Local
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides novel immunoregulatory factor designated IL-X which has been isolated Mycoplasma and polunucleotides encoding such polypeptides. The polynucleotide is useful for augmenting proliferation of B and T lymphocytes. The present sequence is Mycoplasma fermentans II X mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide, useful for augmenting proliferation {\tt T} lymphocytes.
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                14-JAN-2003.
                                                                                            Immunoregulatory factor;
                                                                                                                       Mycoplasma
                                                                                                                                                 06-MAY-2004
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                                          US6506892-B1
                                                                  Mycoplasma fermentans
                                                                                                                                                                             ADK68537;
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: :|: | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                          ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERNQÍKÍÍGÍÐF-ÐIETEYKW--FYSLQFNIKESAFTTGYAIÁSWLSEQ---DESKRVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERKSEIMAAKADANKH------FGLNMAIVTAGGTVNDNSFNQSSWEAI
                                                                                                                                                                                                                                                                     RLEAIISAINK 401
                                                                                                                                                                                                                                                                                              SLDKLITDINK 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNDESNÍSFKEKDISKYTTTNANGKQVVKNAELLKLKPILITDEGKIDDKSFNÓSAFEAL
                                                                                                                                                                                                                                                                                                                        IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
                                                                                                                                                                                                                                                                                                                                                                                                     FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 14; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blazar
                                                                                                                    fermentans IL-X mature protein
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26.9%;
                                                                                            IL-X;
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Pred. No. 2.2e-20;
89; Mismatches 155;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 404 AA;
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(BLAZ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide, useful for augmenting proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1997;
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BLAZAR
                                                                                                                                                                                                SFGGGAFFGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT 226
RLEAIISAINK
                                                                                               ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                                                                                                                                               VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                                                                                                      VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 281
                                                                                                                                                                                                                                                                                                                        QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 162
                                                                                                                                                                                                                                                                                                                                                NNDESNISFKEKDISKYTTTNANGKOVVKNAELLKLKPILITDEGKIDDKSFNOSAFEAL
                        SLDKLITDINK
                                               IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
                                                                      VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE
                                                                                                                       FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 381
                                                                                                                                                                      IAS------KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 331
                                                                                                                                                                                                                                              ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA
                                                                                                                                                                                                                                                                       TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 222
                                                                                                                                                                                                                                                                                                 KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAYREEL
                                                                                                                                                                                                                                                                                                                                                                         NERKSEIMAAKADANKH--------FGLNMAIVTAGGTVNDNSFNQSSWEAI 102
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Result
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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                    4 US-09-182-625F-9
US-09-182-625F-16
US-09-182-625F-14
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US-09-114-000C-6004
US-09-071-035-78
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                 Sequence 9, Appli sequence 14, Appl sequence 15, Appl sequence 8, Appli sequence 8, Appli sequence 8, Appli sequence 8, Appli sequence 6004, Appli sequence 6005, Appli sequence 6005, Appli sequence 6005, Appli sequence 6, Appli sequence 4, Appli sequence 16, Appli sequence 15, Appli sequence 2074, Appli sequence 2774, Appli sequence 277
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| 3 US-09-791-74 3 US-09-793-6-4AP-5 4 US-09-952-267B-5 3 US-09-074-658-75 4 US-09-206-942-47 9 US-09-206-942-47 1 US-08-409-995-4 1 US-08-685-467-4 3 US-09-777-155-3 3 US-09-777-152-3 3 US-09-797-862-3 4 US-09-669-974-3 5 US-09-684-707-4 5 US-09-268-347-47 5 US-09-268-347-47 5 US-09-336-447B-13 6 US-09-336-447B-13 7 US-09-323-992A-2 | 1164 | 873 | 873 | 2354 | 2353 | 2353 | 2353 | 2353 | 2353 | 1912 | 1912 | 1079 | 1073 | 941 | 892 | 892 | 1861 | |
| US-08-790-912-4 US-09-336-447A-5 US-09-952-267B-5 US-09-974-658-75 US-09-206-942-49 US-09-206-942-47 US-08-685-467-4 US-08-685-467-4 US-09-685-974-33 US-09-689-974-33 US-09-684-707-4 US-09-684-707-4 US-09-684-707-4 US-09-684-707-4 US-09-268-347-47 US-09-336-447A-13 US-09-952-267B-13 US-09-952-267B-13 | w | 4 | w | w | 4, | 4. | ω | ω | w | w | <u>ب</u> | 4. | .4 | w | 4 | W | N | |
| | US-08-923-992A-2 | US-09-952-267B-13 | US-09-336-447A-13 | US-09-268-347-47 | US-09-684-707-4 | US-09-797-862-33 | US-09-669-974-33 | US-08-913-942-4 | US-09-377-155-33 | US-08-685-467-4 | US-08-409-995-4 | US-09-206-942-47 | US-09-206-942-49 | US-09-074-658-75 | US-09-952-267B-5 | US-09-336-447A-5 | | |
| | Appli | 13, Appl | 13, Appl | 47, Appl | 4, Appli | 33, Appl | 33, Appl | 4, Appli | 33, Appl | 4, Appli | 4, Appli | 47, Appl | 49, Appl | 75, App1 | 5, Appli | 5, Appli | 4, Appli | |

ALIGNMENTS

| Q | р Q | D Qy | р <i>Q</i> | B 8 | D Qy | B 8 | Query Ma Best Loo Matches | RESULT 1 US-09-182-6; Sequence ; Patent No ; Patent No ; Patent No ; Patent III.E OF ; TITLE OF ; TITLE OF ; TITLE REF! ; CURRENT ; CURRENT ; CURRENT ; PRIOR FII ; NUMBER OO ; SEQ ID NO ; LENGTH ; ORGANISH US-09-182-6; |
|--|--|--|--|--|---|---|--|--|
| 352YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI 401 | 293 AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL- 351 | 244 KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLL 292 | 184 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI 243 | 124 EGKYSSLANTNKNVWVLSGFOHGDAFTRWLKIPBNKOLFTEKNIIILGIDWTDTENVIPT 183 | 64 EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123 : : :: :: | 5 IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS 63 | Query Match 17.1%; Score 393.5; DB 4; Length 428; Best Local Similarity 26.8%; Pred. No. 1.7e-27; Matches 126; Conservative 101; Mismatches 174; Indels 69; Gaps 20; | US-09-182-625F-9 US-09-182-625F-9 Sequence 9, Application US/09182625F Sequence 0. 6506892 GENERAL INFORMATION: APPLICANT: Webb, Andrew C. APPLICANT: Webb, Andrew C. TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gr. TITLE OF INVENTION: Regulation FILE REFERENCE: BLAZ-101XC1 CURRENT APPLICATION NUMBER: US/09/182,625F CURRENT FILING DATE: 1998-10-29 PRIOR APPLICATION NUMBER: US 60/063,701 PRIOR FILING DATE: 1997-10-29 NUMBER OF SEQ ID NOS: 16 SEQ ID NO 9 LENGTH: 428 LENGTH: 428 TYPE: PRT ORGANISM: Mycoplasma fermentans US-09-182-625F-9 |

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RESULT 3
US-09-182-625F-14
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GENERAL INFORMATION:
APPLICANT: Webb, Andrew
APPLICANT: Blazar, Beve
                                                     Sequence 14, Application Patent No. 6506892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blazar, Beverly A.

TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in TITLE OF INVENTION: Regulation FILE REFERENCE: BLAZ-101XC1

CURRENT APPLICATION NUMBER: US/09/182,625F

CURRENT FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: US 60/063,701

PRIOR PILING DATE: 1997-10-29

PRIOR FILING DATE: 1997-10-29

NUMBER OF SEQ ID NOS: 16
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ORGANISM: Mycoplasma
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                                                                                                                                                                                                                                                                                                                            AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-
                                                                                                                                                                                                                                                                                                                                                                          LYYNOXH--KSSKIYHTSPVKLDSGF-----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                                             KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               --FYSLOFNIKESAFTTGYALASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVKNAEL----LKLKPILITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
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                                                                                                                                                                                                                                   LEKEEGYKPYVVKDKKADKKWSHFGTQ------KEKWIGVAENHFSNTEEQAKINNKI
                                                                                                                                                                                                                                                                                                      SVAGPAT -- FETVRLANKGOYVIGVDSDQGMI -- QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAYREELERNQIKIIGIDF-DIETEYKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK 425
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                                                                                                                                                               KEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
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                                                                                                                                                                                                                                                                    ----YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
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   Beverly A.
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Pred. No. 3.3e-27;
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APPLICANT: Webb, Andrew C.
APPLICANT: Blazar, Beverly A.
APPLICANT: Blazar, Beverly A.
TITLE OF INVENTION: Polynucleotides Encoding
FILE OF INVENTION: Regulation
FILE REPERENCE: BLAZ-101XC1
CURRENT APPLICATION NUMBER: US/09/182,625F
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR PILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 15
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; ORGANISM: Mycoplasma US-09-182-625F-15
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US-09-182-625F-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 14
LENGTH: 404
                                                                                                                                                                                                                                                                                Sequence 15, Application US/09182625F Patent No. 6506892 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Polynucleotides Encoding TITLE OF INVENTION: Regulation FILE REPERENCE: BLAZ-101XC1 CURRENT APPLICATION NUMBER: US/09/182,625F CURRENT FILING DATE: 1998-10-29 PRIOR APPLICATION NUMBER: US 60/063,701 PRIOR FILING DATE: 1997-10-29
                                   LENGTH: 40
TYPE: PRT
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                                                      404
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                                                                                                                                                                                                                                                                                                                                                                                                                     RLEAIISAINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAS------KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNDESNISFKEKDISKYTTTNANGKOVVKNAELLKLKPILITDEGKIDDKSFNOSAFEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDKLITDINK 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGVAENHFSNTEEQAKINNKIKEAIKMFKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF-----TAGEKMNT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA 173
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Query Match

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RESULT 5
US-09-583-110-2686
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PRIOR FILLING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILLING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2686
LENGTH: 363
                                                                                                                                                                                                                                                              Query Match 9.8%; Score 225; DB 4; Length 363; Best Local Similarity 24.8%; Pred. No. 3.9e-12; Matches 110; Conservative 61; Mismatches 150; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2686, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.9%; Pred. No. 2e-26; Matches 116; Conservative 88; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-07A
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 RLEATISAINK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ-----KEKW 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 SFGGGAFÞGVTTFNEGFAKGILYYNQKH--KSSKÍYHTSPVKLDSGF----TAGEKMNT 226
  117 DSSTAELE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 VINNVLSSTPADVKYNPHVILSVÄGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR 282
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                                                                                                                                                                                           1 MKKKIKWNKFLGLGLVFPLSAIATIS-AGCWDKETTKEEKSADNQNKQITDVSKISGLVN 59
                                                                                                      ERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGEITSV 116
                                                                                                                                                             MNKK----QWLGLGLV----AVAAVGLAACGNRSSRNAASSSDVKTK------
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                                                 -----AAIVTDTGGVDDKSFNOSAWEGLOAWGKEHNLSKDNGFTY 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                                                                  Matches
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-85
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Ar
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 VLIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 TSILKNIGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGND 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 I-SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 IILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
h 8.8%; Score 203; DB 3;
Similarity 25.7%; Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSTLKQVGTTVKDI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOSTSEADYANNLQQAAGSYNLI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKLATEAISEAKKEFEEKTKTIP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD 236
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette,
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                                                                                56; Mismatches 144; Indels 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SNKAEKGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FGVGFALHNAVEEAAKEHTDLNY 138
                                                                                                                                 Length 328;
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RESULT 7
US-09-536-784-8
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Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                  TELEFAX: (301) 309-
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/961,083 FILING DATE: OCT-30-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K----AVEDAKAKILDGSVKVP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STLKOVGTTVKDI-----SNKAERGEFPGGO---VIVYSLKDKGVDLAVINLSEEGK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSTSEADYANNLQQAAGSYNLIFGV-----GFALNNA-----VKDAAKEHTDLNYV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILKNLGYSVFSVLSDLYTKKSNSRNLAGFBFGKKSATVYLGIKDRFVDIADTSLEGNDK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTYF
                                                                                                                               TOPOLOGY: linear
                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue
                                                                                                                                                                                          LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences,
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  8.8%;
25.7%;
                                                                                                                                                                                                                                                             309-8512
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                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e, 3.50 inch, 1.4Mb storage
486/33
Score 203; DB 4;
Pred. No. 3.4e-10;
                                                                                       NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae Antigens and Vaccines
                    Length 328;
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US-09-107-532A-5084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5084, Application US/09107532A
PATENT NO. 6583275
PATENT INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                   INFORMATION FOR SEQ ID NO: 5084:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 FILING DATE: 30-Jun-1998 PRIOR APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997 ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 73: CORRESPONDENCE ADDRESS:
                                                                                                                                               TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 SSTABLE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSTSEADYANNLQQAAGSYNLIFGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNOSSWEAIQQLGA---LTGGEITSVD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K----AVEDAKAKILDGSVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLATEAISEAKKEFEEKTKTIP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLKQVGTTVKDI-----SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEGK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SPAVIDFIAGYLAGIKAWNLKNSDKKIKITIDKIEINLGFDVQDISIKERLEQIASKDK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTYF
                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
                                          TYPE: amino acid
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Walthan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                              ENGTH: 374 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                             (781)893-8277
                      linear
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                                                                 acids
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                                                                                                                                                                                              GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFALNNA-----VKDAAKEHTDLNYV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144;
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Sequence 6004, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

SOFTWARE: Patentin version 3.1

SEQ ID NO 6004

LENGTH: 362
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                                                                                                                                                                      Matches 107;
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...374
SEQUENCE DESCRIPTION: SEQ ID NO: 5084:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 SNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 AKSLNESGDKKVWVIGVDRDQSDEGEYTLNGEKKNFTLTSTLKAVG----TVVEDLAQKS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 I--IANQNDR--YLIGVDTDQS-----LVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 TYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 NIDOALNAGFKTIFGIGYKLKPAIQEQATNNTGTNFVIIDDVIDGLD--NV-----VSA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 -----LSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILG--IDWTDTENVIPTGRYINL 189
                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 ALITOTGGVDDRSFNQSAWEGLEKWGK------DQGLSRGNDGFQYFQSSNESDYIF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWV- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
SEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAE 122
                                                                                                                   KKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASEVRKTLEIPEMPDK 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIA----SKDKPSTLLAVAGPLTEIFSD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFKDNEASYLAGVAAAY-----TTETNVVGFIGGVKGEVIDRFDAGFKAGVDA-GA 210
                                                                       RKVKQAKFLGLGLAAVALTIGLAACGGNSKKNANTKGDPQHSVVMVTD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ISGDVKVPETPEE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGK-----PPGGEHTVY-GLKEDGVGLTEGQLSDEAKK----AVDEAKEKI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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25.2%;
                                                                                                                                                                 8.7%; Score 199.5; DB 4;
23.3%; Pred. No. 8.5e-10;
tive 69; Mismatches 152;
                                                                                                                                                                                                                                                                                    faecalis
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                                                                                                                                                                 Indels 131;
                                                                                                                                                                                                             Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
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RESULT 10
US-09-071-035-80
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                                                                                    US-09-071-035-80
                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
  Query Match
Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gil H.
                                                                                                 LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 IPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 LEGKYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKKLATEAIS-EAKKEFEEKTKTIPAEEVRKTLEIPEMP 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GKNNVASATFRDNESAYLAGVAAA-----NTTKTNKVGFIGGVEGPVIGRFQAGF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQSNEASDYTSNIDQAISSQFKTIFGIGYLLKNAVVDAADANPETNFVLI----DDTVN- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TAG--IDDKSFNQSAWEGMQEWG--KEHKLPEGPQGYAY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LTTEALSDOAKTAVKEAKEQIISGDVK----VPDQP 362
7.9%; Score 182; DB 4; Length 339; ilarity 25.4%; Pred. No. 3.1e-08; Conservative 51; Mismatches 139; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gil H. Choi
VENTION: Enterococcus faecalis Polynucleotides and Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            version 6.2
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Indels 116;

Gaps

20

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, MOLECULE TYPE: US-09-071-035-78
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US-09-071-035-78
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PATENT NO. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
                                                                                              TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                 CLASSIFICATION: DATA: PRIOR APPLICATION NUMBER:
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gil H. (
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                          LENGTH: 361 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Human Genome Sciences,
T: 9410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20850
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                                                                                361 amino acids
                                                                                                                              (301) 309-8504
(301) 309-851
                                                                                                                                                                                                                                                                                                                                                                                               PE: Diskette, 3.5
HP Vectra 486/33
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                                   linear
               protein
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                                                                                                                                                                                                36,373
                                                                                                                                                                                                                                                                                                                                                                                                                      3.50 inch, 1.4Mb
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: ENTERCOCCUS FAECALIS FO FILE REFERENCE: 032796-032
CURRENT FILLING DATE: 1990-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6005
LENGTH: 375
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US-09-134-000C-6005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6617156
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               Matches
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Best Local &
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                Local Similarity
194
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                                231 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS 289
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                                                                                                                                                                                                                                                                                             104;
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                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                                       61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                       GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 230
                                                                                                                                                                                ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 170
                                                                                                                                                                                                                      KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNQSSWEGLQAWGKEHDLPEGSKGYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGKALAAAMYQNGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKVGFVGGEEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDWIDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 230
VVIDRFQAGFEKGV-ADAAKELGKEITVDT
                                                                     DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA-----ISSAADANPDTNFVLI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNQSSWEGLQAWGKEHDLPEGSKGYAY 84
                                                                                                                                               IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA----ISSAADANPDTNFVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDLTDGYL -- NDKT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK-----FPGGEHLVY-GLKDGG
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                               Score 182; DB 4;
Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 182; DB 4;
Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                             Mismatches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 361;
                                                                                                                                                                                                                                                                                                                              Length 375;
                                                                                                                                                                                                                                                                                             Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                        -NETKTNKVGFVGGEEG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116;
 KYAASFADPA
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                                                                                                                                               148
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 232
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US-08-396-957A-5
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                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664
FILING DATE: 05-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: SIMPSO
                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,245
FILING DATE: 19-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                            HYPOTHETICAL: N
                                                                                                                                             MOLECULE TYPE: pr
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 01-MAFCLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                         ORGANISM:
                                                                                                                                                                                                                                       ENGTH:
                                                                        STRAIN: Sh-2-82
[NDIVIDUAL ISOLATE:
                                                                                                                                                                                     OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341
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                                                                                                                                                                                 unknown
                                                                                                         Borrelia burgdorferi
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                                                                                                                                                                protein
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ANTIGENIC PROTEINS AND
GENES ENCODING SAME OF BORRELIA BURGDORFERI.
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                                                                                                                                                                                                                                                                                        APPLICANT: Webb, Andrew C.
APPLICANT: Blazar, Beverly A.
APPLICANT: Blazar, Beverly A.
APPLICANT: Blazar, Beverly A.
TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in Cell Gr
TITLE OF INVENTION: Regulation
FILE REFERENCE: BLAZ-101XC1
CURRENT APPLICATION NUMBER: US/09/182,625F
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR PRIOR DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09182625F Patent No. 6506892
GENERAL INFORMATION:
                                                                                Query Match
Best Local Similarity
Matches 50; Conserv
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Best Local Similarity
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mycoplasma fermentans
FEATURE:
                                                                                                                                                                                                                                                                             LENGTH: 166
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 PTGRYINLTYKTEEAGWLAGY--ANASFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 -- LANTNKN---- VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 181
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  N
                                   GGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIA 283
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  GGGAFPGVTTFNEGFAKGILYYNOKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVI 54
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                                                                                7.5%; Score 173; DB 4; I
larity 27.3%; Pred. No. 6.6e-08;
Conservative 37; Mismatches 56;
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                                                                                                                        Length 166;
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                                                                                  Indels
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US-08-396-957A-4
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                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,9572
FILING DATE: 01-WAR-1995
CLASSIFICATION LATA:
APPLICATION NUMBER: 08/020,245
PRIOR APPLICATION NUMBER: 08/020,245
FILING DATE: 19-FEB-1993
CLASSIFICATION NUMBER: 09/664,731
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664,731
FILING DATE: 05-WAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-WAY-1990
ATTORNEY/AGENT INPORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                       TELEFAX: (212) 751-684
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SIMPSON, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                       NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                            HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                        MOLECULE TYPE:
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ADDRESSEE: MORGAN &
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                             ORGANISM:
STRAIN: S
                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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Sh-2-82
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ANTIGENIC PROTEINS AND
GENES ENCODING SAME OF BORRELIA BURGDORFERI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANELLE:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 7.0%;
Local Similarity 22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: OTHER INFORMATION: p39' prot OTHER INFORMATION: sequence.
                                                                                                                                                                                           315
                                                                                                                                                                                                                                                                                                          143
326
                                  435 DKQQESLDKLITD 447
                                                                          286
                                                                                                              375 LGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                    KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL 314
                                                                                                                                                                                                                                                                                                          YIAAKL-----SKTGKIGFLGGIEGEIVDAFRYGYEAGAKYAN-----KDIKISTO 188
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-SNKESYEKFLKE 337
                                                                          YGLKEGVVGFV----RNPKMISF-----
                                                                                                                                                     IGVDEDQAYL---APDNVITSTTKDVGRAL----NIFT--SNHLKTNTFEGGK---LIN 285
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                                                                            ELEKEIDNLSSKIINKEIIVP-----
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Search completed: December 18, 2004, 01:28:35 Job time : 33.9611 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
Published Applications AA:*

1: /cgn2 6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2 6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2 6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

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11: /cgn2 6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2 6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

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18: /cgn2 6/ptcdata/2/pubpaa/US10N_PUB.pep:*

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19: /cgn2 6/ptcdata/2/pubpaa/US10N_PUB.pep:*

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Gapop 10.0 , Gapext 0.5
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2299
1 MKKKIKWNKFLGLGI
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1548.256 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | 10 | _ | 80 | 7 | o. | 5 | 4 | ω | N | μ | Result |
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| 188.5 | 188.5 | 203 | 214.5 | 214.5 | 217.5 | 217.5 | 217.5 | 217.5 | 217.5 | 221 | 223 | 232.5 | Score |
| 8.2 | 8.2 | 8.8 | 9.3 | 9.3 | 9.5 | 9.5 | 9.5 | 9.5 | 9.5 | 9.6 | 9.7 | 10.1 | Query Match Length DB |
| 347 | 347 | 328 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 344 | 350 | 350 | ength |
| 17 | 15 | ø | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 10 | 17 | BB |
| US-10-474-792-180 | US-10-451-337-8 | US-09-765-272-8 | US-10-451-337-42 | US-10-451-337-16 | US-10-451-337-41 | US-10-451-337-40 | US-10-451-337-39 | US-10-451-337-14 | US-10-451-337-12 | US-10-451-337-6 | US-09-769-787-132 | US-10-474-792-166 | ID |
| Sequence 180, App | Sequence 8, Appli | Sequence 8, Appli | Sequence 42, Appl | Sequence 16, Appl | Sequence 41, Appl | Sequence 40, Appl | Sequence 39, Appl | Sequence 14, Appl | Sequence 12, Appl | Sequence 6, Appli | Sequence 132, App | Sequence 166, App | Description |

| ь ц л ц | | | 42 | 41 | | | | 37 | 36 | 35 | 34 | | | | | | | | | | | | | 21 | 20 | 19 | 18 | 17 | 16 | 15. | 14 |
|---------------|--------------|---------------|----------|----------------------|---------|----------------------|-------------------|--------------|---------------|----------|-------------------|----------------------|------|--------------|-------|---------|--------------|----------------|-------------------|------|-----------------|-------------------|------------------|-----------|------------|----------------------|-------------------|-------------------|-----|---------|------|
| | 117.5 | 117.5 | 118 | 118 | 1 | 118.5 | 118.5 | \mathbf{r} | 119 | 119 | 120 | ٠ | ٠ | ٠ | 122.5 | 122.5 | | • | • | ٥. | | • | 141.5 | 150 | 156 | 169 | 173 | 182 | 182 | 182 | 182 |
| 5 C | | | | | | | | | | | | | | | | 5. 3 | | | | 5.7 | | | | | | | | | | 7.9 | 7.9 |
| 6641 | 1079 | $\overline{}$ | 1849 | 896 | 571 | 2872 | 1963 | 902 | 892 | 776 | 719 | 2457 | 1104 | 852 | 2285 | 2059 | 2045 | 1031 | 998 | 496 | 1787 | 1786 | 889 | 223 | 797 | 357 | 166 | 361 | 361 | 339 | 339 |
| 15 | 14 | 14 | 16 | 5 | 15 | 15 | 15 | 16 | 10 | 14 | 15 | 15 | 9 | 15 | φ | 17 | 15 | 15 | 15 | 16 | 15 | φ | 10 | 10 | 14 | 15 | 9 | 14 | 9 | 14 | 9 |
| -10-282-122A- | -10-193-764- | -10-193-764-4 | -10-637- | US-10-282-122A-60816 | -10-282 | US-10-282-122A-60137 | -10-282 | 7-963-1055 | -09-952-267-5 | -10-238- | 10- | US-10-282-122A-49854 | 9 | -10-282-122A | 09-93 | -10-474 | 0-282-122A-7 | -10-282-122A-5 | 10-282-122A-70 | -10- | US-10-415-253-2 | 09-7 | US-09-952-267-15 | 769-736- | 156-761-10 | US-10-282-122A-60484 | US-09-760-541-6 | US-10-206-576-78 | -7 | 06-576- | 035- |
| e 7058 | e 43 | e 45, App | e 2, 1 | e 60816, | . T | e 60137, | Sequence 73978, A | e 109 | O | e 571 | Sequence 2, Appli | e 498 | | 0 | Ņ | e 62, | (D | 54611, | Sequence 70450, A | 432, | e 2 | Sequence 3, Appli | 1 | e 48, App | e 10907, | æ | Sequence 6, Appli | Sequence 78, Appl | 78, | a | 80, |

T A GIMMENT

| APPLICANT: Olmsted, Stephen APPLICANT: Zagursky, Robert APPLICANT: Mickbarg, Elliot APPLICANT: Nickbarg, Elliot AP |
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| Gape KSEIM : AELEGI STSESI |

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APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
ITITLE OF INVENTION: Protesins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
VUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 132
LENGTH: 350
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-769-787-132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.7%; Score 223; DB 10; Best Local Similarity 24.8%; Pred. No. 4.5e-08; Matches 110; Conservative 63; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 132, Application No. US20 GENERAL INFORMATION
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  224
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                                                                                                                                                                                   168 IILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407
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                                                                                                                                                                                                                                                                                    117 DSSTAELE------GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNI 167
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                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                     I-SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKD
                                                                                                                                                                                                                                                                                                                                                                                                                  MNKK----QWLGLGLV----AVAAVGLAACGNRSSRNAASSSDVKTK-----
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                                                                                                                                                              VLIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGG
                                                                                                                                                                                                                                                                                                                                                      ERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGEITSV 116
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                                        KPSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFF
                                                                                                                                                                                                                                               FOSTSEADYANNLOQAAGSYNLIFGV-----GFALNNA-----VKDAAKEHTDLNY 125
                                                                               IESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD
---IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVL
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D. US20030091577A1
                                                                                                                                                                                                                                                                                                                               -----AAIVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 122;
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US-10-451-337-6
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Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10451337
Publication No. US20040097706A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HAMEL, JOSEE
APPLICANT: RIGUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREETOCOCCUS PYOGENES ANTIGENS ATTILE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard
APPLICANT: HAMBL, Josee
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                                                                                                                                                                                                                                        177
327
                                   401
                                                                           283
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                                                                                                                                                           223
                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                        134 --NV-----ASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRF 176
                                                                                                                                                                                                                                                                                                                                                                177
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                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GKYSSLANTNKNVWVLSGFQ--HGDAFTRWLK-----IPENKQLFTEKNIILGIDWTD 176
                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 SKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGQSWGKEMGLQKG---TGFDYFQSTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AKADANKHFGLMMAIVTAGGTVNDNSFNOSSWEAI---QQLGALTGGEITSVDSSTAELE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGND 393
                                                                                                                                                                                    LAVAGPLTEIFSDIIANQN----DR-YLIGVDTDQ--SLVYT----KTKNKFFTSILKNL 340
                                                                                                                                                                                                                                                                            AGYLAGIKAWNIKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTL
                                                                                                                                                                                                                                                                                                                                                              TENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFI 236
                                                                           GKAVQLINKQVADK--
                                                                                                             GYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEA 400
                                                                                                                                                         QAAGGTGAGVFNEAAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEV 282
                                                                                                                                                                                                                                        EGFEAGVKS---
                                                                                                                                                                                                                                                                                                                                                                                                        SEYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNGVKFVIIDDIIEGKD--- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFIGLG----LASVAVLSLAACGNRG-----
IKEAKAKIKSGDIKVP 342
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                                   ISEAKKEFEEKTKTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 221; DB 15; ilarity 26.4%; Pred. No. 6.1e-08; Conservative 56; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bernard R.
                                     416
                                                                                                                                                                                                                                        ----VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG 329
                                                                               FPGGK--TTVY-GLKDGGVEIATT----NVSKEAVKA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 344;
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APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephane
APPLICANT: RIBAULT, PALTICK
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
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APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: HODDEUR, Bernard R.
APPLICANT: HAWEL, Josee
APPLICANT: HAWEL, Josee
APPLICANT: RIEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FAPLICATION NUMBER: US 60/256,940
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-10-451-337-14
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US-10-451-337-12
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Publication No. US20040097706A1
PUBLICATION:
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LENGTH: 330
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Local Similarity 28.3%; Pred. No. 1e-07;
nes 102; Conservative 47; Mismatches 142; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 LINKQVADKK-----FPGGK--TTVY-GLKDGGVETATT----NVSKEAVKAIKEAK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 GAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VKS------VDDTİQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 IKAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 DNVASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AAKADANKHFGLNMAIVTAGGTVNDNSFNOSSWEAIQQLGALTG-GEITSVDSSTAELEG 125
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US-10-451-337-39
; Sequence 39, Application US/10451337
; Publication No. US20040097706A1
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; ORGANISM: S.
US-10-451-337-39
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SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 39
LENGTH: 330
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Best Local Similarity
Matches 102; Conserv
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SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 330
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HAMEL, JOSEE
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 1286-24PCT
FILE REFERENCE: 1286-24PCT
FILE REFERENCE: 1280-24PCT
FILE
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APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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126 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 LINKQVADKK-----FPGGK--TTVY-GLKDGGVETATT----NVSKEAVKAIKEAK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 LTEIFSDIIANQNDR-----YLIGYDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIILGIDWTDTENVIPT 183
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                                                                                                                                                                                                        AAKADANKHFGLNMAIVTAGGTVNDNSFNOSSWEAIQQLGALTG-GEITSVDSSTAELEG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES 78
                                                                                                                           ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                     ; Score 217.5; DB 15; ; Pred. No. 1e-07; 47; Mismatches 142;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                      Length 330;
                                                                                                                                                                                                                                                                                             69;
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; LENGTH: 330
; TYPE: PRT
; ORGANISM: S. |
US-10-451-337-40
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APPLICANT: RIGUX, Stephane
APPLICANT: RHEAULT, Patrick
FITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS ANT
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-242FT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR TILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-451-337-40
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Publication No. US20040097706A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 40
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APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard
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                                             346 SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 405
                                                                                                                                                                                                                                                                                               129 DNVASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 IKAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGP 297
                                                                                                                                             298 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 345
                                                                                                                                                                                                                                            243 IKAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 9.5%; Score 217.5; DB 15; Length 330; al Similarity 28.3%; Pred. No. 1e-07; 102; Conservative 47; Mismatches 142; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                    126 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 AAKADANKHEGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTG-GEITSVDSSTAELEG
  LINKQVADKK-----
                                                                                               GAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQ
                                                                                                                                                                                                                                                                                                                                            GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKQVADKK-----FPGGK-TTVY-GLKDGGVEIATT---
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                                                                                                                                                                                                                                                                                                                                                                                         EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES
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                                                                                                                                                                                               -----VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT
-FPGGK--TTVY-GLKDGGVEIATT----NVSKEAVKAIKEAK
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; LENGTH: 330
; TYPE: PRT
; ORGANISM: S.
US-10-451-337-41
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publication No. US20040097706A1

GENERAL INFORMATION:
APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
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APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, PATTICK
FITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                  US-10-451-337-16; Sequence 16, Application US/10451337; Publication No. US20040097706A1
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US-10-451-337-41
GENERAL INFORMATION:
APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 41
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                                                                                                                                                                                                                                                   286 LINKQVADKK-----FPGGK--TTVY-GLKDGGVEIATT----NVSKEAVKAIKEAK 330
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                                                                                                                                                                                                                                                                                              SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT
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APPLICANT: HAMEL, JOSEE
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, PALTICK
TITLE OF INVENTION: STREETCOCCCUS PYOGENES /
TITLE OF INVENTION: CORRESPONDING DNA FRAGM
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940

PYOGENES ANTIGENS

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RESULT 10
US-10-451-337-42
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; TYPE: PRT
; ORGANISM: S. pyogenes
US-10-451-337-16
                                                                                                                                        Query Match
Best Local S
Matches 102
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NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/10451337 Publication No. US20040097706A1
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 42
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mouse
-10-451-337-42
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HAMEL, JOSSEE
APPLICANT: RICHAY, STEPFICK
APPLICANT: REBAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 12806-24PCT
                                                                                                                                                                                                                                                                                                     ENGTH: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 LINKQVADKK-----FPGGK--TTVY-GLKDGGVEIATT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 IKAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 DNVASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG 242
  126 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
                                                                                                                                          102; Conservative
                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 AAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTG-GEITSVDSSTAELEG 125
                                                                                         67 AAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTG-GEITSVDSSTABLEG 125
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKS------VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASKGGAAGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES 78
                                              ASKGGAAGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 214.5; llarity 28.3%; Pred. No. 1.70 Conservative 46; Mismatches
                                                                                                                                     9.3%; Score 214.5; DB 15; Length
28.3%; Pred. No. 1.7e-07;
tive 46; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143; Indels
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                                                                                                                                                                                 Length 330;
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118 SSTAELE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 168

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-765-272-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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US-09-765-272-8
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Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                         Matches
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/765,272
PILING DATE: 22-Jan-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VKS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 LINKQVADKK-----FPGGK--TTVY-GLKDGGVEÍATT----NVSKEÁVKÁÍKÉÁK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 GAGVFNEAKAINEKKSEADKVWVÍGVDRDOKDEGKÝTSKDGKEANFVLASSIKEVGKAVO 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
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                                            RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGEITSVD 117
  RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTYF 58
                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences,
                                                                                           Conservative
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                                                                                    8.8%; Score 203; DB 9; Length 328; 25.7%; Pred. No. 1.2e-06; ative 56; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            (301)
                                                                                                                                                                                                                                                                                                                 amino acids
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                                                                                           84;
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APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: HAMEL, Josee
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephane
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24 PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT APPLICATION NUMBER: US/0/256,940
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
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US-10-451-337-8
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                                                                                                                                                                                                                                                                                                                             Matches 113;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 347
                                                                                                                                                                                                                                                                                                                                           Match 8.2%; Score 188.5; DB 15; Local Similarity 25.7%; Pred. No. 1.5e-05;
 172
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                              231 AVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPST
                                                                                                                                                             114 TSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTR-WLKIPENKQLFTEKNIIIL 170
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                                                                                                                                 77
                                                                                                                                                                                                                            61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLG---ALTGGE----I 113
                                                                                                                                                                                                                                                                                              ۳
                                                                                             GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 230
                                                                                                                             QSANESEFTTNLE---SAVTNGYNLVFGI-GFPLHDAVEKVAANNPDNH--FAIVDDVIK 130
                                                                                                                                                                                                                                                                                 MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLKQVGTTVKDI-----SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEGK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI 228
VVKRFEKGFEAGVKSVD------DTIKVRVAYAGSFADAAKGKTIAAAQYAEGADV
                                                             G-----QKNV-----ASITFSDHEAAYLAGVAAAK-----TTKTKQVGFV-GGMEGD
                                                                                                                                                                                                                                                              MNKKV-----MSLGLV--STALFTL-GGC-----TNNSAKQTTDNS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGGI
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                              -LKIAMITNQTGIDDKSFNQSAWEGLQAWGKENKLEKGKGYDYF 76
                                                                                                                                                                                                                                                                                                                           59; Mismatches 150; Indels 117;
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US-10-474-792-180
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Best Local Similarity
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; ORGANISM: Streptococcus pyogenes US-10-474-792-180
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TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
SEQ ID NO 180
LENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Olmsted, Stephen
APPLICANT: Zagursky, Rober
APPLICANT: Nickbarg, Ellio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 TSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTR-WLKIPENKQLFTEKNIIIL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNONKQITDVSKISGLVNE 60
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--AIEAAKKAIIEGTITVP
                                                          TEAISEAKKEFEEKTKTIP 416
                                                                                                                                                                           KNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLA 397
                                                                                                                                                                                                                                                                                                                                                       VVKRFEKGFEAGVKSVD------DTIKVRVAYAGSFADAAKGKTIAAAQYAEGADV 221
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Nickbarg, Elliot
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25.7%; Pred. No. 1.5e-05;
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                                                                                                                       QFPGGQITTF-GLKEGGVSLTTDALTQDTKK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
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CITY: Rockville
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                                                                                                                                                                                                                VVIDRFQAGFEKGV-ADAAKELGKEITVDT---
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                                                                                                                                                                                                                                                                                                                                                         IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA-----ISSAADANPDTNFVLI 112
VDLTDGYL--NDKT------KEAVKTAKDKVISGDVKVPEKPE 339
                                 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 431
                                                                    KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK--
                                                                                                    KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 381
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9410 Key West Avenue
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o. US20020045737A1
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(301) 30
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HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 182; DB 9; Length 339;
Pred. No. 4.4e-05;
51; Mismatches 139; Indels 116;
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TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: S
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US-10-206-576-80
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Publication No. US20030017495A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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197 KGKALAAMYQNGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY-
                                                                                                                                                                                                                                                                                  113 ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 170
                                                                                                                                                                                                                                                                                                                                                                 61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGE----
                                     AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS 289
                                                                                                                                                                                                                                                                                                                        KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNOSSWEGLQAWGKEHDLPEGSKGYAY 62
                                                                               VVIDRFQAGFEKGV-ADAAKELGKEITVDT
                                                                                                                                                             DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKVGFVGGEEG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
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FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows
SOFTWARE: ASCII Text
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STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                                                                                                          IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA-----ISSAADANPDTNFVLI 112
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                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 182; DB 14;
Pred. No. 4.4e-05;
1; Mismatches 139;
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                                                                                 -KYAASFADPA
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      255
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| Search Job tim | Db | ξŞ | Ъ | γQ |
|--|---|--|--|---|
| Search completed: December 18, 2004, 01:44:02 Job time : 106.236 secs | 305 VDLTDGYLNDKTKEAVKTAKDKVISGDVKVPEKPE 339 | 382 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 431 | 256 KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDKFPGGEHLVY-GLKDGG 304 | 327 KTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 381 |

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OM protein - protein search, using sw model
                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
```

Run on: December 18, 2004, 01:15:13 ; Search time 27.349 Seconds (without alignments)
1586.669 Million cell updates/sec

US-09-676-249D-2 2299 1 MKKKIKWNKFLGLGLVFPLS.....KQPDKQQESLDKLITDINKN 451

Title: Perfect score:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | ហ | 4 | ω | N | <u>,</u> | No. | Result |
|--------------------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|---------------|
| 127.5 | 129.5 | 129.5 | 130 | 132 | 132 | 140.5 | 140.5 | 141 | 141.5 | 143.5 | 147 | 156.5 | 162 | 164 | 168.5 | 169 | 169.5 | 174 | 178 | 181.5 | 182 | 185.5 | 187.5 | 195.5 | 207 | 219 | 223 | 554.5 | Score | |
| ა | 5.6 | 5.6 | | | | | 6.1 | 6.1 | 6.2 | | | 6.8 | 7.0 | 7.1 | 7.3 | 7.4 | 7.4 | 7.6 | 7.7 | 7.9 | 7.9 | 8.1 | 8.2 | 8 5 | 9.0 | 9.5 | 9.7 | 24.1 | Match | Q uery |
| 763 | 1558 | 1140 | 484 | 657 | 547 | 337 | 337 | 379 | 539 | 384 | 353 | 591 | 339 | 524 | 525 | 357 | 360 | 357 | 341 | 359 | 353 | 350 | 516 | 357 | 350 | 374 | 350 | 461 | Length | |
| N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | _ | <u>,,</u> | N | N | N | N | N | N | B | |
| A82863 | B71603 | S73786 | B90524 | S73428 | E29504 | B97374 | AH2591 | H75318 | D82886 | I40867 | G70147 | D64204 | F70147 | D82944 | C82914 | AD1248 | H70147 | AH1610 | E70147 | F72418 | H71340 | C70009 | C82946 | D96986 | F86804 | C97965 | G95097 | B90555 | Ħ | |
| hypothetical prote | | | hypothetical prote | ğ | mercury(II) reduct | Deinococcus radiod | membrane lipoprote | membrane lipoprote | conserved hypothet | hypothetical prote | basic membrane pro | membrane lipoprote | basic membrane pro | hypothetical membr | conserved hypothet | CD4+ T cell-stimul | basic membrane pro | CD4+ T cell-stimul | basic membrane lip | basic membrane pro | membrane lipoprote | ABC transporter (1 | hypothetical prote | probable lipoprote | basic membrane pro | conserved hypothet | lipoprotein [impor | ABC transporter xy | 읽 | |

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346 TSIVKNIAFPVYQILLALLTKDEESVILKEGNDKFLGS---NPKNLVLKRGLSAKFVNIT 402

| 45 1 | | 43 | 42 1 | | | | | | | | | | 32 | 31 | 30 |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| | 119.5 | 121 | | | | | | | 123.5 | | | 124.5 | | 126 | |
| 5.2 | 5.2 | 5.3 | 5.3 | 5.3 | ω | 5.3 | 5.4 | 5.4 | 5.4 | 5.4 | 5.4 | | | | |
| 627 | 350 | 1546 | 2346 | 2285 | 553 | 553 | 1223 | 1031 | 626 | 322 | 2269 | 556 | 1635 | 326 | 349 |
| 2 | ນ | N | N | | | | | N | N | N | | N | N | N | N |
| A41609 | F70139 | G90603 | T13829 | T12796 | AH0640 | SMEBH1 | E88451 | C81302 | C25035 | F84236 | T28677 | H82301 | AI0452 | G95857 | F84246 |
| dnaK-type molecula | exported protein (| lipoprotein (impor | Tpr homolog - frui | probable transglyc | flagellar hook-ass | flagellar hook-ass | protein K10D2.1 (i | probable type I si | colicin Ia - Esche | ABC transporter (1 | rhoptry protein - | peptide ABC transp | hemolysin [importe | hypothetical prote | hypothetical prote |

ALIGNMENTS

| C;Genetics: A;Genetics: A;Gene | RESULT 1 B90555 B90555 ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: B90555 R;Chambaud, I; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084 A;Accession: B90555 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-461 <kur> A;Cross-references: UNIPROT:Q98QL5; GB:AL445566; PID:g14089760; PIDN:CAC13519.1; GSP</kur> |
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| IKWNKFLG IKWNKFLG MKLNKK | olecus sidu coss- cperi neti neti neti neti |
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| 277 286 | 유 성 |
| | B 8 |

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C;Species: Streptococcus pneumountage C;Date: 03-Aug-2001 #sequence_revision 03-Aug-C;Accession: G95097 R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 Science 293, 498-506, 2001
conserved hypothetical protein spr0747 [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: C97965 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dei e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <KUR>
A;Cross-references: UNIPROT:Q97RHO; GB:AE005672; PIDN:AAK74976.1; PID:g14972319;
A;Experimental source: strain TIGR4
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGG
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                                                                                                                                                                                                                                                                                                                      ---IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNKK----QWLGLGLV----AVAAVGLAACGNRSSRNAASSSDVKTK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQSTSEADYANNLQQAAGSYNLIFGV------GFALNNA-----VKDAAKEHTDLNY 125
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24.8%; Pred. No. 2.4e-06;
tive 63; Mismatches 148
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S.L.; L
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M.R.;
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Radune, D.; Holtzapple,
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S.; DeHoff, B
, P.; McAhren,
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pneumoniae.
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Query Match Best Local Sim Matches 107;

Similarity

9.0%;

Score 207; DB 2; Pred. No. 2.3e-05; 2; Mismatches 156;

Length 350;

Indels

118;

Gaps

20;

Conservative

62;

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A; Experimental : C; Genetics: A; Gene: bmpA
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J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C97965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <KUR>
A;Cross-references: UNIPROT:Q8DQC2; GB:AE007317; PIDN:AAK99551.1; PID:g15
C;Genetics:
A;Gene: spr0747
                                                                                                                                                                    R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weenome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86804
                                                                                                                                                                                                                                                                                                               basic membrane protein A [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis (Strain C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
                                                  A;Cross-references: UNIPROT:Q9CFM9;
A;Experimental source: strain IL1403
                                                                                                A;Molecule type: DNA
A;Residues: 1-350 <STO>
                                                                                                                                           A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KK----AVEDAKAKILDGSVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I-SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IILGIDWTDTENVIPTGRYINLTYKTEBAGWLAGYANASFLAKKFPSDPTKRSAIVIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AAIVTDTGGVDDKSFDQSAWEGLQAWGKEHNLSKDNGFTY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 219; DB 2;
; Pred. No. 4.7e-06;
62; Mismatches 150
                                                                         GB:AE005176; PID:g12724428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SNKAEKGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                              PIDN: AAK05536.1;
                                                                                                                                                                                                                                                                         Weissenbach,
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| Qy 1 MKKKIKMNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE 60 2 IKKKT | nt-Producing Bacte .1; PID:915023581; .357; 121; Gaps 20; | CDRFVDIADTSLEGNDKK 395 | Qy 172 IDWTDTENVIPTGRYINLTYKTERAGWLAGYANASFLAKKFPSDPTKR8AI-VICGGISP 230 Db 130 SVIKDQRWVASATFADNESAYLAGVAAAKATKTNKIGFIGGMQSD 174 Qy 231 AVTDFIAGYAAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPST 290 Qy 175 VITRFEKGYEAGAKSVNPDIKVDVQYAGSFSDAAKGKTIAAAMYGAGDDV 224 Qy 291 LLAVAGPL-TEIFSDIIANQNDR-YLIGVDTDQSLVYTKTKNKFFTSIL 337 Qy 18 | MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISG |
|--|---|--|---|--|
| | rium Clc GSPDB:G | x., Leee, | | |
| B Q B Q B Q | B & B & B & B | submitted A; Descript A; Reference A; Accession A; Status: A; Molecule A; Residues A; Cross-re A; Experime C; Genetics A; Genetic A; Genetic A; Genetic A; Genetic A; Genetic A; Genetic | Oy Db RESULT 6 C02946 C02946 hypothet C;Specie C;Date: C;Access R;Glass | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| 227GISPA-VTDFIAGYLAGIKAWNLKNSDKKTKITTDKIBINL | 1 MKKKIKWNKFLGIGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE 60 | to GenBank, February 2000 ton: The complete sequence of Ureaplasma urealyticum: Alternate views e number: A82870 n: C82946 preliminary type: DNA 1-516 <gla> 1-516 <gla> ferences: GB.AE002100; GB:AF222894; NID:g6898946; PIDN:AAF30417.1; GS! ferences: GB.AE002100; GB:AF222894; DB:g6898946; PIDN:AAF30417.1; GS! ferences: GB.AE002100; GB:AF222894; DB:g6898946; PIDN:AAF30417.1; GS! ferences: GB.AE002100; GB:AF222894; NID:g68989946; PIDN:AAF30417.1; GS! ferences: GB.AE002100; GB:AE002100; GB:AE00</gla></gla> | 406 K | AVTDFIAGYLAGI : :: : LINKFLSGYIAGA TLLAVAGFLTEIF : VYHAAGGAGIGVF SVLSDLYTKKSNS : : NTVKDLVKGKK |

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R;Kuntt, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Masuda, S.; Maucel Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wingat, A.; Yamamoto, H.; Yamanoto, K.; Yasumoto, K.; Yasta, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Reference number: A6580; MUID:98044033; PMID:9384377

A;Reference number: A6580; MUID:98044033; PMID:9384377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:005252; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15143
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-350 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 8.1%; Score 185.5; DB 1
Similarity 24.8%; Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIVTAGGTVNDNSFNOSSWEAIQQLGALTG-----GEITSVDSSTAELEGKYSSLANTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNM
                                                                                                        LAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEF-----EEK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLFKTLDKKPVVDGYLDVKKET 413
TKTIPAE 418
                                                                                                                                                            KKEDPKRDVWVIGVDKDQYAEGQVEGTDDNVTLTSMVK----KVDTVVEDV-TKKASDGK
                                                                                                                                                                                          KKTKITTDKIEINLGFDVQDT--STKERLEQIASKDKPSTLLAVAGPL-TEIFSDIIAN-
                                                                                                                                                                                                                                                                                                                                                                                       QEGSFLVGVAAAL-----SSKSGKIGFVGGMESELIKKFEVGFRAGVQAVNPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                              EEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAGIKAWNLKNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDLIYGVGYLMEDSIS---EIADQR-----KNTNFAIIDAVVDKDNV-----ASITFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGID-WTDTENVIPTGRYINLTYKT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMVTDVGGVDDKSFNQSAWEGIQAFGKENGLKKGKNGYDYLQSKSDADYTTNLNKLAREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTILGACGNSE--KSSGSGEGKNK-------
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                                                                                                                                                                                                                                                                           ----AVVEVKYAGGFDKADVGKATAESM----YKSGVDVIYHSAGATGTGVFTE-AKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter yufN
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                                                    TLTYGLDQDGVGISPSKQNLSDDVI--KAVDKWKKKIIDGLEIPATEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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RESULT 9 F72418

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A;Gene: tmpC; TP0319
A;Start codon: GTG
C;Superfamily: ABC transporter yufN
C;Superfamily: ABC transporter yufN
C;Keywords: blocked amino end; lipoprotein; membrane protein; thiolester bon
C;Keywords: aignal sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <MAT>
F;21-353/Product: membrane lipoprotein tmpC #status predicted <MAT>
F;21/Modified site: fatty acylated amino end (Cys) (in mature form) #status
F;21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 281, 375-388, 1998
A,Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A,Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71340
A,Status: nucleic acid sequence not shown; translation not shown
A,Status: nucleic acid sequence not shown; translation not shown
A,Status: nucleic acid sequence not shown; translation not shown
A;Molecule: UNA
A;Molecule: Lype: DNA
A;Residues: 1-353 <COL>
A;Cross-references: UNIFROT:P29724; GB:AE001211; GB:AE000520; NID:g3322582; PIDN:AAC6530;
A;Cross-references: UNIFROT:P29724; GB:AE001211; GB:AE000520; NID:g3322582; PIDN:AAC6530;
A;Experimental source: strain Nichols
A;Schouls, L.M.; van der Heide, H.G.U.; van Embden, J.D.A.
Infect: Immun. 59, 3316-3346, 1991
A;Title: Characterization of the 35-kilodalton Treponema pallidum subsp. pallidum recombi
A,Reference number: A43595; MUID:91372962; PMID:1894360
A,Accession: A43595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-10,'A',12-158,'R',160-353 <SCH>
A; Cross-references: GB:X57836; NID:948838; PIDN:CAA40968.1;
A; Note: this protein is shown to incorporate palmitic acid
C; Genetics:
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les 86; Conserv
343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGVA-AALKAKE----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VACGSFLVEA-----VIETSARFPKQKFLVIDAVVQDRDNV-----VSAVFGQNEGSF 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW 198
                                                             EIP
                                                                                                                                                                                                                                                                                                                         ANQNDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAGYANASFLAKKFPSDPTKRSAI--VIGG--GISPAVTDFIAGYLAGIKAWNLKNSDKK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGMVTDSGDIDDKSFNQQVWEGISRFAQENNAKCKYVTASTDAEYVPSLSAFADENMGLV 101
                                                                                                                                                                                                                                                            LNGQDVWVIGVDRDQYMDGVYDGSKSVVLTSMVKRA-----DVAAERISKMAYDGSFPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG----PLTEIFSDII 306
                                                                                                                                                                                           EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL 424
                                                                                                                                                                                                                                                                                                                                                                                          -----PDIQVVVEVANTFSDPQKGQALAAKLYDSGVNVIFQVAGGTGNGVIKEARDRR
                                                                                                                          ----GQSIMFGLEDKAVGIPE----
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 182; DB 1; I
Pred. No. 0.00077;
9; Mismatches 134;
                                                                                                                              -ENPNLSSAVMEKIRSFEEKI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 353
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RESULT 10
E70147

basic membrane lipoprotein B (bmpB) - Lyme disease spirochete
C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence revision 13-Feb-1998 #text_change 09-Jul-2004
C;Date: 13-Feb-1998 #sequence revision 13-Feb-1998 #text_change 09-Jul-2004
C;Date: 13-Feb-1998 #sequence A.R.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
son, D.; Feterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Howman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-359 <ARN>
A;Cross-references: UNIPROT:Q9WXV7; GB:AE001696; GB:AE000512; NID:g4980582; PIDN:AAD351
A;Experimental source: strain MSB8
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A;Cross-references: UNIPROT:Q45011; GB:AE001143; GB:AE000783; NID:g2688279; PIDN:AAC6675
A;Experimental source: strain B31
R;Simpson, W.J.; Cieplak, W.
                                                                                                 A,Status: preliminary, nucleic acid
A,Molecule type: DNA
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                                                                              A;Residues: 1-341 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 94
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;Date: i1-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYLAGIKAWNLKNSDKKTKI----TTDKIEINLGFDVQDTSTKERLEQI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QILP--NVLTFTFKEQEAAFLVGYVAAAM-----TKTGMVGFVGGIPIPPVERFRY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGIS-PAVTDFIA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDS-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISE----AKKEFEEKTKTIP-AEEVRKTLEIPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEAAREKFSA-LAGSDKLVDLIDYYTTNGKGFFAIGVDMDQDYM---APGAVLTSAMKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYEAGIKTYSVLHK-KNVKILRGYTODFEDPKKGKDLAMSQFAEGADIVFHASGACGNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSDYIPNLSKAAEEADLVFAVGFMMTNDLFKVAKQYPDT-----YFVGIDITPPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAELEGKYSSLANTNKNYWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTE- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKFLVISLMIFAVALFGFKVIMVTDVGGLGDKSFNDGTWAGIKQAAEELGIEAKVIQSYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAELLYLEKLMKEGTLKVPETQEELDAFEVPQI
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                                                                                                                            sequence
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                                                                                                                                  shown;
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on, D.;
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Vugt,
B.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-232,'A',234-317,'V',319-341 <RES>
A;Residues: 1-232,'A',234-317,'V',319-341 <RES>
A;Cross-references: GB:I24194; NID:g508420; PIDN:AAA72407.1;
R;Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A;Title: Conservation of gene arrangement and an unusual orga
A;Reference number: I40241; MUID:95111614; PMID:7812434
A;Accession: I40242
                                          CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria innocua (strain Clip1 C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AH1610
                                                                                                                                           RESULT
AH1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-44,'A',46-179 <RE2>
A;Cross-references: GB:L35050; NID:9516591; PIDN:AAC41402.1; PID:9551744
C;Superfamily: basic membrane protein C
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A;Title: Nucloetide sequence and analysis of the gene in Borrelia burgdorferi encoding the A;Reference number: 140289; MUID:94327086; PMID:8050720
A;Accession: 140290
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Similarity 26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSS--
                                                                                                                                                                                                                                          KVLERKIINKEIIVP
                                                                                                                                                                                                                                                                                       KTIPAEEVRKTLEIP 427
                                                                                                                                                                                                                                                                                                                                         IKNNNV-----WEGGK---VVQMGLRDGVIGLPNAN-----
                                                                                                                                                                                                                                                                                                                                                                                      TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGLAGIGVIETAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGYESGAKYAN-KDIEIISEYSNSFSDVDIG-----RTIASKWYSKGIDVIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTGRYINLTYKTEEAGWLAGY -- ANASFLAKKFPSDPTKRSAIVIG -- GGISPAVTD-FI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV 78
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Pred. No. 0.0013;
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Fsihi, H.,
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AH1610
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1610
A,Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPROT:Q92BW7; GB:AL592022; PIDN:CAC96656.1; PID:g16413898; GSPDB:GNA;Experimental source: strain Clip11262
C;Genetics:
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Voss, H.; Wehland,
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A;Cross-references: GB:AE001144; GB:AE000783; NID:g2688291; PIDN:AAB91505.1; PID:g268829
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100, MUID:98065943, PMID:9403685
A;Accession: H70147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Gazland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       basic membrane protein D (bmpD) homolog - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 113-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C;Accession: H70147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: tcsA
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                             ;Experimental source: strain B31;Superfamily: basic membrane protein C
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Best Local Similarity
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                                                                                                                                                                                             65 IMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SGVVLGACGSSSDDKKS-----GDDKSSKDFTVAMVTDTGGVDDRSFNQSAWEGIQKFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 SGLV-----NERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLG
                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                   GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAG
                                                                                                                         GKYSSLANTNKN-VWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
                                                                                                                                                               VACSSSDDGKSEAKTVSLI-VDGAFDDKGFNESSSKAIRKLKADLNINIIEKASTGNSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP 430
                                                                                       GDIANLEDGNSNLIWGI-GFRLSDIL--FQRASENVSV----NYAI--IEGVYDEIQIPK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDFAKADKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALT----GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK
                  -NLLNISFRSEEVAFLAGY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEYGLDKDAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD-----IKVPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQWDEGKVTANDGKDYNVTLTSEIKRVDIAV----DDLAT-----RTKAGDFPGGTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQ-----SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --DTSTKERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TTKTNKVGFVGGVKGAVIDRFEAGFTAGVKA-----VNPNAQIDVQY
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                                                                                                                                                                                                                                       7.4%;
larity 25.4%;
Conservative 6
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24.2%; Pred. No. 0.0024;
ative 62; Mismatches 137;
                                                                                                                                                                                                                                     ;; Score 169.5; DB 2;
;; Pred. No. 0.0045;
64; Mismatches 137;
                  FASKASKTGKIGFVGGVRGKVLESFMYGYEAG
                                                                                                                                                                                                                                                                                                                                                                                                      not shown;
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                                                                                                                                                                                                                                       137;
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                                                                                                                                                                                                                                                                                                                                                                                                      translation not shown
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Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ak, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: AD1248
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AD1248
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C;Superfamily: ABC transporter yufN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q48754; GB:NC_003210; PIDN:CAC99466.1; PID:g16410817; GSPDB:(A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-357 <GLA>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK-IPENKQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LETGV--LDGGK---TMFLGLKEDGLGLVLNENLKSNYSEIYNKSL 331
DAVGLSE---
                                                     RFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
                                                                                                                VTANDGKDYNVTLTSEIKRVDIAV----
                                                                                                                                                                                                                             DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK 271
                                                                                                                                                                                                                                                                                      ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDTDQ-----
                                                                                                                                                                                                                                                                                                                                           KVGFVGGVKGTVIDRFEAGFTAGVKA-------VNPNAQIDVQYANDFAKA
                                                                                                                                                                                                                                                                                                                                                                                                AIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVO---DTSTK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIVDDTI-----DDRDNVVSIG-----FKDNDGSYLVGVVAGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNOSSWEAIQQLGALT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKYAN-----SNIKVVSQYVGTFGDFGLG-----RSTASNM----YRDGVDIIFAAAG-L 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IXAWNLKNSDKKTKITTDKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĠTDGYNYLQŚASEADYK-----TNLNTAVRŚDYDLIYGIGYKLKDAIEEVSKQKPKNQF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILGACGSSSDDKKSSDDKSSKDF--TVAMVTDTGGVDDRSFNQSAWEGLQKFGKANDMEK 76
                                                                                                                                                                  -SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD
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--HODNISKDVLAKVE---EYKOKIVDGD----IKVPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 169; DB 2;
Pred. No. 0.0048;
                                                                                                             -EDLAT----RAKAGDFPGGTK---IEYGLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 357;
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Voss, H.; Wehland,
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14

hypothetical membrane lipoprotein UU226

[imported]

Ureaplasma urealyticum

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hypothetical membrane lipoprotein UU016 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: D82944
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views A;Reference number: A82870
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A;Accession: C82914
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: C82914
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cass
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A;Molecule type: DNA
A;Residues: 1-525 <GLA>
A;Cross-references: GB:AE002101; GB:AF222894; NID:g6898957; PIDN:AAF30421.1; GSPDB:GN001
                        A; Molecule type: DNA
A; Residues: 1-524 <GLA>
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A;Experimental source: serovar 3; biovar 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIASKDKPSTLLAVAGPLTEIFSDIIANQNDR-YLIGVDTDQSLVYTKTKNKFF--TSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIAGYLAGIKAWNLKNSDKKTKITTDKIE---INL-----GFDVQDTSTKER--LE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGKDRIASITYRADQAAFLAGIAAAYYLNSNQNVFGKD----NKLTWGGFVGIHLPSTTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NTALVELSKAGHQYLIDAIKLSGLKEVNDYKTIVEIIQEDPLFKLLSQIGTKKLDEVAT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNLGYSVFSVLS--DLYTK------KSNSRNLAGFEFGKKSATVYLGIKDRFVDI 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YASKIQDGARMLGLISFRHKNPISKYFNSPKDNQ---QVSAVLI-----DEIYDLQ 119
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A;Experimental source: serovar 3; biovar C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TAELEGKYSSLANTNKNVWVLSGFOHGDAFTRWLKIPENKOLFTEKNIIILGIDWTDTEN 179
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                                                                                                                                                                            -----VYTKTKNKFFT---SILKNLGYSVFSVLSDLY--TKKSNSRNLAGFEFGKKSAT 372
                                                                                                                                                                                                              GSFKPDEEGATNIINDLITKKADVILPVAGPQTNLATSIVSNATDPSVIIGVDTAQELDD 281
                                                                                                                                                                                                                                            ------DKPSTLLAVAGPLTEIFSDIIANQND-RYLIGVDTDQSL---
                                                                                                                                                                                                                                                                                        TFIQGFKLGVQWANEKLKDK-----EIN----QEDANGSKKKWMNVEQVFASKYVA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LEDFYAKPAGDDSLGYHRT------
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KGTTKLEDLATKTSDGWVLKDSEKNKSFSELQKLL
                               KTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLI 445
                                                                     SL---
                                                                                                       VYLGIKDRFVDIADTS------LEGNDKKLATEAISEAK-----
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Copyright (c) 1993 - 2004 Compugen Ltd.
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| TDKIEINLGFDVQDTSTKERLEQIASKD | PTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGIS : : : : | SSLANTNKNVWYLSGFOHGDAFTRWLKIPENKQLFTEKNIIILGIDW | NKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQOLGALTG-GEITSVDSSTAE - - | ISAGCWDKETTKEEKSADNQNKQITDVSKISGI ; VSCGETDKEGKIIRIFDNSF | Score 706; DB 2; Length Pred. No. 2.7e-35; 7; Mismatches 145; Inde: | Potential. Ag 243-5 protein. Ag 243-5 protein. ; 9AEEAB11620CB22F CRC64; | σ. | sma_p48. | 400(1995). ding; IEA. | of a novel molecule, $A_{\underline{c}}$ nation of the complete | ., Ohta T., Fukuda S., | 1970: | cutes; Mycoplasmataceae; My | annotat | e update) | PRT; 457 AA. | | ALIGNMENTS | ACSU 31 | 097L60 06MUL7 CAE76664 079YM5 08X8S6 08X919 |
| SKDKPSTLLAVAGPLT 299 | IGGGISPAVTDFIAGY 239 : FGGGHGAGVTDFIAGF 233 | IIILGIDWTDTEN 179 : ::: /IIVAVDWDLSKEDKD 173 | GEITSVDSSTAELEGKY 127 :: :: DRVSQETNNQSELIGKY 113 | KISGLVNERKSEIMAAKADA 72 : : : NSFVKDRQABIEKA 54 | 1 457; els 46; Gaps 16; | - | | | | y 243-5 derived nucleotide | Sugimura K., | | Mycoplasma. | | | | | | OBixq5 brucella su OBp2u0 streptcoccc Opprd3 ureaplasma O05252 bacillus su O732t4 bacillus ce Aas42731 bacillus O311357 borrelia ga | clostrial mycoplasm 64 mycoplasm 54 mycopla streptoco streptoco enteroco |

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Q98QL5;
01-OCT-2001
01-OCT-2001
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL445564; CAC13519.1; PIR; B90555; B90555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., S
Moszer I., Dybvig K., Wrobiewski H., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02608; Bmp; 1.
PRINTS; PR01733; LIPPROTEIN48.
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Nucleic Acids Res. 29:2145-2153(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blanchard A.;
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                                                                                                                                                                                                                                                                                                         KSQNKEAENQHKLDNYINSAVKDLEQNYKVALDRGYTTWILTGFQQGNEIENFLNDENNL
                                                                                                                                                                                                                                                                                                                                                                                                                    VTETQKIVENKIKQASLETQK-----VVLITADGNIDDKSFNQQVYESQKTLKDFVDKAY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLNK--KLFSTLPVAALAIALPATF-----VSCAQNPNKTNSNLDSSKITDLLSQKE
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                                                                                                                   RSAIVIGGGISPAVTDFIAGYLAGIKAWN--LKNSDKKTKITTDKIEINLGFDVQDTSTK
                                                                                                                                                                                                                                                  QLFTEKNIIILGIDWTDTEN-VIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTK 218
                                                                                                                                                                                                                                                                                                                                                                      TS----
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                          ERLEQIASKDKPSTLLAVAGPLTEIFSDII---ANQNDRYLIGVDTDQSLVYTKTKNKFF
                                                                                RAISAFGGGDFAGVTDFLNGFFEGIRAWNSEAENANKKVKIVSENLVLDTGF-IPNAEKN
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                                                                                                                                                                                                                                                                                                                                                                ------VDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENK 159
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30.3%; Pred. No. 6e-26;
tive 88; Mismatches 1
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05-JUL-2004
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Unspecified sugar ABC transporter binding protein.
OrderedLocusNames=MMOB0360;
Mycoplasma mobile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren B.W., Stange-Thomann N., Smith C., DeCaprio D., Fis Butler J., Calvo S., Elkin T., FitzGerald M.G., Hafez N., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AE017337; AAT27522.1; -. InterPro; IPR008107; Mycoplasma_p48.
PRINTS; PR01733; LIPPROTEIN48.
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STRAIN=163K / ATCC 43663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2118;
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438
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                                                                                                                                                                                                                                                                                                                                                                        QQLGALTG--GEITSVDSSTA---ELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                NONKOITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNOSSWEAI
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                          ------EEKTK---TIPAEEVRKTLEIPEMP--DKQPDKQQESLDKLITDIN
                                                                              RNLAGFEFGKKSATVYLGIKDR-----FVDIADTSLEGNDKKLATEA-----ISBAKKEF
                                                                                                                                                                      NTGFAV----TPEAATAIQSIVGSGTQVVFPVAGSLTTLTVNSISQENSGQFVIGVDSDQ
                                                                                                                                                                                                NLGFDVQDTSTKERLEQIASKDKPST--LLAVAGPLTEIFSDIIANQND-RYLIGVDTDQ
                                                                                                                                                                                                                                                          KRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNS-----DKKTKITT-DKIEI
                                                                                                                                                                                                                                                                                      NRAEFIRKQVIIVAIDWTTNLELVPPGQFISINYRTQESSWIVGNAVAKFISDNHNNN--
                                                                                                                                                                                                                                                                                                                                             LEIGRQTGKPGNFSFAETTAGTPDQLQRQYDQALFFNHKFWVLTGFQQDGAFQNWLQIGN
                                                                                                                                                                                                                                                                                                                                                                                                  NTGLRVTDNQVFRDLVASREAEFATQRVANNSLFNSKTLLITAGGVVNDLSFNOSINEAL
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                                                                                                              AKAFSPDLAKLFFSSVEKNVAGTTYAALASLYLGTVSTDPFFNITGSSSRFIPVTEKNNS
                                                                                                                                        SLYYTKTKNK-FFTSILKNLGYSVFSVLSDLY------TKKSNS
                                                                                                                                                                                                                             -RTFNTFGGGAFPEVTNFNAGFLQGILDFN--NSTFLEPGETSITDNKKLSFTPGDIINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                     --LANADITKGFVESTEPVDFVGFSKSALGGKITQSLVQANVGRSFAEVADEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 467.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 165;
----VQIPNFSGGPSTPEQIPNPLNELIKKIN
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Best Local Similarity
Matches 141; Conserv
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AAT27522;
24-MAY-2004 (TrEMBLrel. 27, Created)
24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Unspecified sugar ABC transporter binding protein.
MMOB0360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaffe J.D., Church G.M.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017337; AAT27522.1; -.
SEQUENCE 491 AA; 52817 MW; 2D1C707687771B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren B.W., Stange-Thomann N., Smith C., DeCaprio D., Fis Butler J., Calvo S., Elkin T., FitzGerald M.G., Hafez N., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=163K;
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LAASLALFNKNKAKIIATIP-----VOIPNFSGGPSTPEQIPNPLNELIKKIN 485
                                                                                                                                                                        RNLAGFEFGKKSATVYLGIKDR-----FVDIADTSLEGNDKKLATEA-----ISEAKKEF
                                                                                                                                                                                                                                         RAFSPDLAKLFFSSVEKNVAGTTYAALASLYLGTVSTDPFFNITGSSSRFIPVTEKNNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RTFNTFGGGAFPEVTNFNAGFLQGILDFN--NSTFLEPGETSITDNKKLSFTPGDIINI
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                                                                                                                      -Lanaditkgfvestepvdfvgfsksalggkitqslvqanvgrsfaevadey
                                                           EEKTK---TIPAEEVRKTLEIPEMP--DKQPDKQQESLDKLITDIN 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Score 467.5; DB 2
29.7%; Pred. No. 1.5e-20;
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N., Kodira C.D.,
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RESULT Q6E5B5

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Best Local Similarity
Matches 139; Conserv
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O6E5B5;

O1-OCT-2004 (TrEMBLrel.:

O1-OCT-2004 (TrEMBLrel.:

O1-OCT-2004 (TrEMBLrel.:
                                                                                                    01-NOV-1999
01-NOV-1999
01-MAR-2004
                                                   Name=p48;
Mycoplasma agalactiae
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

ROBALÍ S., Albertí A., Robino P., Pittau M.;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ

EMBL; AY557344; AAT64137.1; -.
                                                                                                                                          Q9X775;
                                                                                                                                                     Q9X775
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              SEQUENCE FROM
                                                                                        P48 membrane
  MEDLINE=20002620; PubMed=10531294;
                                     NCBI_TaxID=2110;
                                                                                                                                                                                                                                             431
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                                                                                                                                                                                                                                            DKQPDKQQESLDKLITDINK 450
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                                                                                       (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
s lipoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                       PRELIMINARY;
           N.A.
                                                                                                                                                                                                                                                                      TSGLLDSKNDEIANKALEEATKYYESK-----KAEIQKTLSGQLEEAKKALG
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                                                   Mollicutes; Mycoplasmataceae; Mycoplasma
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28,
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; Pred. No. 8.6e-19;
93; Mismatches 179;
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Last sequence update)
Last annotation update)
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Best Local Similarity
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O52311;
O1-JUN-1998 (TrEMBLrel. 06, C:
01-JUN-1998 (TrEMBLrel. 06, L:
01-MAR-2004 (TrEMBLrel. 26, L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
 STRAIN=PG18;
Rawadi G., I
                      SEQUENCE FROM N.A.
                                      Bacteria; Firmicutes; NCBI_TaxID=2115;
                                                             Membrane lipoprotein P48v. Mycoplasma fermentans.
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Pittau
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465 AA;
 Dyer K.,
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51149 MW;
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                                                  Mollicutes; Mycoplasmataceae;
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                                                                                  Last
Last
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Pred. No. 1.8e-1
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60AD5448CFE03C96 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE ,
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378
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                                                                                                                               NFESAYNSALSAGHKIWYLNGFKHOOSIKOY--IDAHREELERNQIKIIGIDF-DIETEY
KIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
                                 AISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
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                                                                  LILEKEEGYKPYVVKDKKADKKWSHFGTQ
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Pred. No. 1.7
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                                                                  ----KEKWIGVAENHFSNTEEQAKINN
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MEDLINE=99115554; PubMed=9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt Differential posttranslational processing co variation of a major surface lipoprotein and lipopeptide of Mycoplasma fermentans."; Infect. Immun. 67:760-771(1999). EMBL; AR099211; AA016395.1; -... GO; GO.0008289; F.lipid binding; IEA. InterPro; IPR003760; Bmp. InterPro; IPR008107; Mycoplasma_p48. Pfam; PF02608; Bmp; 1.
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Q9RGX5;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=SK5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Macrophage activating lipoprotein-404 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
NCBI_TaxID=2115;
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M161Ag, a Mycoplasma fermentans gene production by human monocytes."; J. Biol. Chem. 273:12407-12414(1998)
                                                                                               Seya T.;
"Structural and functional properties of complement-activating properties of complement activating properties activating properties of complement activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation activation
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MEDLINE-98022661; PubMed-9359703;
MALBUMOTO M., Takeda J., Inoue N., Hara T., Ha
Magasawa S., Akedo H., Seya T.;
"A novel protein that participates in nonself
malignant cells by homologous complement.";
Nat. Med. 3:1266-1270(1997).
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EMBL; AB026157; BAA77211.2; -
GO; GO:0008289; F:lipid binding;
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InterPro; IPR008107; Mycoplasma
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                       SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KOPDKOOESLDKLITDINK
                                                LEKEEGYKPYVVKDKKADKKWSHFGTQ------KEKWIGVAENHFSNTEEQAKINNKI
                                                                                                                    AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Macrophage activating lipoprotein-404 MEDIINE-9911554; PubMed-9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; "Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopsptide of Mycoplasma fermentans."; Infect. Immun. 67:760-7711999). Bacteria; Firmicutes; NCBI_TaxID=2115; Q9RGX4 EMBL; AF099212; AAD16396.1; -. GO; GO:0008289; F:lipid binding; STRAIN-MT-2; SEQUENCE FROM N.A. Mycoplasma fermentans InterPro; 10 IPR003760; PRELIMINARY; Bmp Mollicutes; PRT; IEA Mycoplasmataceae; 429 ₿ update) Mycoplasma

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Macrophage activating l
                                                             variation of a major surface lipoprotein and lipopeptide of Mycoplasma fermentans."; Infect. Immun. 67:760-771(1999). EMBL; AF099210; AAD16394.L; -. GO: GO:0008289; F:lipid binding; IEA. InterPro; IPR003760; Bmp. InterPro; IPR003760; Bmp. InterPro; IPR008107; Mycoplasma_p48. Pfam; PF02608; Bmp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT
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                                     LIPPROTEIN48
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27.0%;
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Last annotation updat
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macrophage activating lipoprotein-404;
B6D08CF975AC3171 CRC64;
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Pred. No. 4.
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.2e-16;
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IKEAIKMFKELPEDFVKYINSDKVLK-----DGNKIDNVSERLEAIISAINK
                                                                                              SVAGPAT
                                                                                                            LYYNQKH--KSSKIYHTSPVKLDSGF-----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                    KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS------
                                                                                                                                                                                             --FYSLOFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFFG
                                                                                                                                                                                                                    GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI
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                                                                                                                                                                                                                                                                                                                     EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
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                                                ILEKEEGYKPYVVKDKKADKKWSHFGTQ
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                         ISEAKKEF-
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429
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                                                                       YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEA
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27.08;
                        EEKTKTI PAEEVRKTLEI PEMPDKQPDKQQESLDKLITDINK
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Pred. No. 4
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    B6D09A8812AC3171 CRC64;
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.2e-16;
                                                KEKWIGVAENHFSNTEEQAKINNK
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Q9RGX7;
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01-MAY-2000 (TrEMBLrel. 13, Createq)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update
01-MAR-2004 (TrEMBLrel. 26, Last annotation upda
SEQUENCE
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                                                                     Lipoprotein; Signal.
SIGNAL 1
                                                                                                                                           Pfam; PF02608; Bmp;
PRINTS; PR01733; LII
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ng confers intraspecies
and a macrophage-activating
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EMBL; AF099213; AAD16397.1; -. GO.0008289; F:lipid binding; IEA.
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01-MAY-2000 (TYEMBLYE1. 13, Last sequence update)
01-MAR-2004 (TYEMBLYE1. 26, Last annotation update)
Macrophage activating lipoprotein-404 precursor.
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InterPro; IPR008107; Mycoplasma_p48.
Pfam; PF02608; Bmp; 1.
PRINTS; PR01733; LIPPROTEIN48.
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                                  99;
                           Score 389.5;
Pred. No. Be-1
99; Mismatches
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Pred. No. 4.5e-16;
"'Amatches 178;
                                                                                                                                           Potential.
macrophage activating lipoprotein-404
; C7A536B409A60132 CRC64;
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                Query Match
Best Local Similarity
Matches 125;
                                                                                                                                Q9R3N6;
                                                                                                                                                                                                                                                                              STRAIN=PG18, M39A, and M70B;
MEDLINE=99115554; PubMed=9916088;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies
"variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999)
                                                                                  Lipoprotein; Signal.
SIGNAL 1
CHAIN 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=malP; Synonyms=malp; Mycoplasma fermentans.
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein MALP-404
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW
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                                                                    428 AA;
 Conservative
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                                                                     47863
                16.9%;
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                                                                    MW;
101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
sor (Macrophage activating lipoprotein-404
              Score 387.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                    macrophage activating lipopeptide
; 59808324E218F03C CRC64;
                                                                                                       Potential.
 Mismatches
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                .5; DB 2;
1.1e-15;
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IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS

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OS Therm
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                                                                                                                                        Query Match
Best Local Sim
Matches 105;
                                                                                                                                                                                                         Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Ya Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of the T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
EMBL; ABO13017; ABAM23740.1; ---
GO; GO:0008289; F:lipid binding; IEA.
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
Complete proteome; Lipoprotein.
Complete proteome; Lipoprotein.
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Q8RCH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Surface lipoprotein. Name=Med; OrderedLocusNames=TTE0457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=MB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21992816; PubMed=11997336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=119072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEÄLKAINKQTGIEINSVEPS-SNF 106
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                                                                    RWRVVLASLLILVL-ALSVVLSGCSSK--TKQEST---QPQQTTEANK----
                                                                                                     KWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNONKOITDVSKISGLVNERKSEI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI 401
                                                                                                                                            Conservative
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NKNF--KVGLVTDVGGINDRSFNQMAYEGLQRAAKELGVTVNVIQSKQMTDYV 95
                                                                                                                                       10.7%; Score 247; DB 2; Length 352; 25.7%; Pred. No. 3.7e-07; Live 62; Mismatches 161; Indels
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                                  LYTKKSNSRNLAGFEFGKKSATVYLGIKDRF----VDIADTSLEGNDK 394
                                                                                                                                                                             IKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIF 302
                                                                                                                                                                                                                                                   RYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIV--IGGGISPAVTDFIAGYLAG
MYFDLKNN----GVGLGKINKDVPQSIIDQVNQLAKDIIDGKIQVSDK 349
                                                                      -GVIKAAQEKNLYAIGVDADQSYL---APDNVLTSAVKRVDVAVYDVIKDALNGNFKSGI
                                                                                                          SDII--ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSD------
                                                                                                                                            AKAVN-----PDIKILINYTNNFNDPAAGKQMALTQISQGAEIIFQVAGGTGE--
                                                                                                                                                                                                                   --ASAMFKEQEVGYLAG--ALAGIVEKEKVGKVKGTNIIGAVGGMQIPPVDRFIAGYQQG
                                                                                                                                                                                                                                                                                         PNLTNFAQQGYDLVISVGPMMHDA-----TEEVSQKFPNTKFLIIDSEITDRPNV---- 145
                                                                                                                                                                                                                                                                                                                              GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTG 184
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Search completed: December 18, 2004, 01:26:31 Job time : 131.457 secs

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Minimum |
Maximum |
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                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1 MWDKETTKEEKSADI
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | ហ | 4 | w | N | _ | Result |
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| 202 | 203.5 | 204 | 206 | 213.5 | 216.5 | 216.5 | 217 | 220.5 | 220.5 | 372 | 375.5 | 375.5 | 378.5 | 378.5 | 379.5 | 379.5 | 642.5 | 692.5 | 693.5 | 702 | 2120 | 2134 | 2134 | 2155 | Score |
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| AAW55066 | ABB54779 | ADK46171 | AAY81632 | ABG66917 | ABG66915 | ABG66916 | ABP27752 | ABG66912 | ABP25843 | AAW22727 | ADK68538 | ADK68537 | ADK68531 | ADK68536 | ABP71709 | AAY05332 | AAP93343 | AAR67582 | AA015867 | AAR40856 | AAU01860 | AA015861 | AAU01859 | AAO15862 | ID |
| Aaw55066 Streptoco | 9 | ۲ | Aay81632 Streptoco | 7 | ū | 0 | | N | Abp25843 Streptoco | Aaw22727 Membrane | Adk68538 Mycoplasm | Adk68537 Mycoplasm | μ | Adk68536 Mycoplasm | Abp71709 M161 anti | Aay05332 Inflammat | Aap93343 Gene enco | Aar67582 Cancer me | Aao15867 Mycoplasm | Aar40856 43kd regr | 0 | Aao15861 Mycoplasm | Aau01859 Mycoplasm | 22 ₹ | Description |

Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae in animals, especially pigs.

Claim 4; Page 20-21; 38pp; English.

The invention comprises the amino acid and coding sequences of Mycoplasma hyopneumoniae mhp3 proteins, the invention also comprises novel apoprotein antigens encoded by the M. hyopneumoniae mhp3 gene. M.

| 202 9.4 358 7 ADC45089 202 9.4 350 6 ABU01234 202 9.4 374 7 ADC95457 195.5 9.1 347 5 ABP20886 195.5 9.1 347 5 ABP25842 179.5 8.3 366 6 ADB09398 178 8.3 339 6 ABU08296 178 8.3 339 6 ABU08296 178 8.3 339 6 ABU13547 178 8.3 339 6 ABU13547 178 8.3 341 2 AAW01758 178 8.3 341 2 AAW01758 178 8.3 361 2 AAV00048 178 8.3 361 2 AAW012547 178 8.3 361 6 ABU3267 178 8.3 361 6 ABU82267 179 8.3 361 6 ABU82267 179 8.3 361 6 ABU82267 170 8.3 361 6 ABU82267 171 8.1 347 5 ABP269913 | 99.4 4 39.0 99.4 4 37.0 8 8 8 8 8 8 8 8 3 3 3 3 4 7 7 5 7 8 6 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 5 7 7 7 7 5 7 7 7 7 5 7 7 7 5 7 7 7 7 5 7 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | . 28 | 27 |
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ALIGNMENTS

RESULT 1 AAO15862 WPI; 2002-742716/81. N-PSDB; AAL50633. King KW, 30-MAR-2001; 2001EP-00303030. Misc-difference Location/Qualifiers 16-JAN-2003 (first entry) 30-MAR-2001; 2001EP-00303030. Misc-difference 422 Mycoplasma hyopneumoniae. Synthetic. Apoprotein antigen; enzootic mycoplasmal pneumonia; mhp3; mutant; mutein; vaccine; Mycoplasma hyopneumoniae infection. Mutant Mycoplasma hyopneumoniae mhp3 protein. AAO15862; AAO15862 standard; protein; 423 (PFIZ) PFIZER PROD INC. 02-OCT-2002. EP1245677-A1 Madura RA, /note= "Wild type Lys replaced by Asn" /note= "Wild type Asn replaced by Leu" note= "Encoded by RGT" Rosey EL;

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RESULT 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 451 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 1; 38pp; English.
                                                                                                                                                                               Sequence 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoprotein antigens encoded by Mycoplasma hyopneumoniae for use in nes to prevent and treat diseases caused by infection with
                                                                                          419;
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                                                                                                                Similarity
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                                                                                                                                                                                                        New apoprotein antigens encoded by mhp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing caused by Mycoplasma hyopneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 417. .422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma hyopneumoniae recombinant MHP3 antigen
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                                                                                                                                                            Claim 4; Page 19-21; 38pp; English
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS03286
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The sequence represents Mycoplasma hyopneumoniae a recombinant MHP3 antigen lacking the first 28 amino acids (the gutative signal sequence MHP3 antigen and its fragments are useful in manufacturing a vaccine i treating or preventing a disease or disorder in an animal, especially pig, caused by M. hyopneumoniae infection e.g. enzootic mycoplasma

sequence).

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RESULT 5
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XX AAR4
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AC AAR4
XX Regi
DT 25-W
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Regression associated antigen; tumour; anti-idiotypic antibodies; antibodies;
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Misc-difference
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tive 0; Mismatches 0;
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11-DEC-1987;
04-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regression associated antigens (RAA's) are identified in material from neoplastic cells by their immunological reactivity with regression associated antibodies from the serum of patients diagnosed as undergoing regression of a tumour. RAA's can be used for tumour immunotherapy and for producing and purifying antibodies which can be used for tumour diagnosis, localisation and therapy. The antibodies can also be used for the production of anti-idiotypic antibodies which can be used in immunotherapy. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 453 AA;
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NDAKONEKALNELIKKIN
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                                                                                                                                                                           NNINIDTGF-ISNDKTATFINGIVNKS--SLVLPVVGSLTSSVVDAIKKSNKDTKYLIGV
                                                                                                                                                                                                   DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII--ANQNDRYLIGV
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                                                                                  YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM--PD 403
                                                                                                                  DTDOSKIFPPA-TVFFTSIEKHLGRTIYEVLTDIWLKKEDSKFLGSFRSFKLTNPANATV
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                         KOPDKOQESLDKLITDIN
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87US-00097910.
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2; Mismatches 146;
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Matches 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel apoprotein antigens encoded by Mycoplasma hyopneumoniae for vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae in animals, especially pigs.
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vaccine; Mycoplasma
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   DTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGK----KSATV 345
                                                                  NNINIDTGF-ISNDKTATFINGIVNKS--SLVLPVAGSLTSSVVDAIKKSNKDTKYLIGV
                                                                                                                           DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII--ANQNDRYLIGV 289
                                                                                                                                                                                                                                   AGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITT 231
                                                                                                                                                                                                                                                                                                                          EFPKFLKQTDSNGKKYSDLLAEKKVIIVAVDWDLSKEDKDLIKAGHFISLLYKTEEAGFI 193
                                                                                                                                                                                                                                                                                                                                                                                      AFTRWLKIPEN-----KQLFTEKNIIILGIDW---TDTENVIPTGRYINLTYKTEEAGWL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFNQSIWEAVLEHYDQIEKTTNLDRVSQETNNQSELIGKYKNFLNGNKNVWILTGFQQGQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFNQSGWEAI----QQLGALTG-GEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETDKEGKII-----RIFD----NSFVKDRQAEIEKA-----KNFDFNTVLLTAGGTVQDK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN
                                                                                                                                                                                              AGYASSKFLAYKFPNDEAKRTIAPFGGGHGAGVTDFIAGFLAGIAKYNNDNPTAKVTISD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Madura RA,
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hyopneumoniae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.2%; Score 693.5; DB 5; 39.0%; Pred. No. 8.5e-47; tive 81; Mismatches 141;
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                                                                                                                                                         Matches
                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        Sequence 432 AA;
                                                                                                                                                                                                                                                                                                        AAQ79124 encodes AAR67582 a protein involved in cancer metastasis, which may be used for the study of metastaic mechanisms, and for clinical tests to determine the presence or absence of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding polypeptide involved in cancer metastasis - useful study of the mechanism of metastasis and in clinical tests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ79124.
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-040317/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAY-1993;
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                                                                                                                                                         168;
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SFNQSGWEAI----QQLGALTG-GEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGD 119
                                                     ETDKEGKII-----RIFD----NSFVKDRQAEIEKA-----KNFDFNTVLLTAGGTVQDK
                                                                                                      ETTKEEKSADNONKOITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN
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                                                                                                                                                         Conservative
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                                                                                                                                                    32.1%; Score 692.5; DB 2; 39.0%; Pred. No. 9.4e-47; tive 81; Mismatches 141;
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Protein
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                                                                                        Tumour regression-associated antigens and antibodies - used in diagnostic tests, monitoring course of therapy and for therapy in cancer patients.
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Pred. No. 1e-42;
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Matches 115
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                             Misc-difference
                                                                                                                                                       Mycoplasma
                                                                                                                                                                                anticancer
                                                                                                                                                                                             M161; antigen; cytotoxic T-lymhpocyte inducer; CTL; cytostatic; cancer;
                                                                                                                                                                                                                           M161 antigen amino acid sequence
                                                                                                                                                                                                                                                        04-APR-2003
                                                                                                                                                                                                                                                                                                               ABP71709 standard;
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                                                                      Misc-difference
                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 17.6%; Score 379.5; DB 2; Similarity 26.7%; Pred. No. 1.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to cytotoxic T-lymhpocyte (CTL)-inducers containing the M161 antigen, its partial peptide or their salt. The activity of CTL-inducers of the invention may be described as cytostatic. The antigen or its peptide fragment are applicable in anticancer agents for the prevention or treatment of cancer. The antigen and its derivative have superior CTL-inductive effect, giving anticancer agents that have low toxicity. The current sequence represents the M161 antigen amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 428 AA;
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                                                                                                                                                                         IAS------KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
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Matches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides novel immunoregulatory factor designated IL-X which has been isolated Mycoplasma and polunucleotides encoding such polypeptides. The polynucleotide is useful for augmenting proliferation of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide, useful for augmenting proliferation of B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-401108/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoregulatory factor; IL-X; lymphocyte proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma fermentans IL-X mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK68536;
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BLAZAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK68530
                                                                                                 VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                                    IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
                                                                                                                                                                                                       SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKWNT
                                                                                                                                                                                                                                                        VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 253
                                                                                                                                                                                                                                                                                                           ERNOIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA 173
                                                                                                                                                                                                                                                                                                                                                              TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                             FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                 KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NERKSEIMAAKADANKH------FGLNMAIVTAGGTVNDNSFNQSGWEAI
ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 14; 42pp;
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Pred. No. 1.3e-21;
98; Mismatches 156
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    which has been isolated Mycoplasma and polunucleotides encoding such polypeptides. The polynucleotide is useful for augmenting proliferation of B and T lymphocytes. The present sequence is Mycoplasma fermentans IL-X precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 428 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide, useful for augmenting proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WEBB/) WEBB A C. (BLAZ/) BLAZAR B A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoregulatory factor; IL-X; lymphocyte proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK68531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tymphocytes.
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DB; ADK68530.
                                                                                                                                                                                                                                                                                 115;
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TEKNIIILGIDWTDTENVIPTGRYINLTYKTEBAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                  NERKSEIMAAKADANKH-------FGLNMAIVTAGGTVNDNSFNOSGWEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLDKLITDIN 421
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                                                                                 KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL 143
                                                                                                                              QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                  NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPILITDEGKIDDKSFNOSAFEAL
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                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Mature IL-X protein"
                                                                                                                                                                                                                                                                                                           17.6%;
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Pred. No. 1.4e-21;
B; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                   Length 428;
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                             Query Match
Best Local Similarity
Matches 115; Conser
                                                                                                                                                                                                                                                                                                                       The invention provides novel immunoregulatory factor designated II-X which has been isolated Mycoplasma and polunucleotides encoding such polypeptides. The polynucleotide is useful for augmenting proliferation of B and T lymphocytes. The present sequence is Mycoplasma fermentans II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide, useful for augmenting proliferation of
                                                                                                                                                                                                                                     Sequence 404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; SEQ ID NO 15; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADK68535
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                                                                                                                                                                                                                                                                                                 X mature protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 SFGGGAPPGVTTPNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT 250
                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEBB A C.
BLAZAR B A.
                                                     NERKSEIMAAKADANKH------FGLNMAIVTAGGTVNDNSFNOSGWEAI 74
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NNDEŚNISFKEKDISKYTTTNANGKQVVKNAELLKLKPILITDEGKIDDKŚFNOŚAFEAL 62
                                                                                                                 17.4%;
ilarity 26.7%;
Conservative E
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                                                                                                             Score 375.5; DB 7;
Pred. No. 2.3e-21;
87; Mismatches 157;
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The invention provides novel immunoregulatory factor designated which has been isolated Mycoplasma and polunucleotides encoding
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                                                                                                Claim 26; SEQ ID NO 16; 42pp; English.
                                                                                                                                                            New isolated polynucleotide, useful for augmenting proliferation {\tt T} lymphocytes.
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(BLAZ/) BLAZAR B A.
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                                                                                                                                                                                                                                                                                                                                                       Blazar BA
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RESULT 15
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XX AAW22
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Matches 115
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                                                                                                                                                                                                                                                                               Membrane protein
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            17-JUN-1997.
                                      JP09157295-A
                                                                              Modified-site
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mes 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAS------KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFGGGAFPGVTTENEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERNQÍKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYÁJÁSWLSEQ---DESKRVVA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAYREEL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERKSEIMAAKADANKH------FGLNMAIVTAGGTVNDNSFNOSGWEAI 74
                                                                                                                                                                                                                                                                                                                                                                                                                              RLEAIISAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDKLITDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPILITDEGKIDDKSFNQSAFEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ-----KEKW
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                                                                                                       /note=
348
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                                                                                                                                                            163
                                                                                                                                                                                   Location/Qualifiers
121
                                                                                                                                                                                                                                                    protein; leukaemia;
                                                                                                                                                                                                                                                                               M161Ag
                                                                note=
                                                                                         note=
                                                                                                                                                                       note= "selenocysteine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.4%; Score 375.5; DB 7; 26.7%; Pred. No. 2.5e-21; tive 87; Mismatches 157;
                                                                                         "selenocysteine"
                                                                                                                  "selenocysteine'
                                                                                                                                             "selenocysteine"
                                                               "selenocysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is a membrane protein designated M161Ag. Oligonucleotide probes for the cDNA were designed from putative N-terminal M161Ag peptide sequences isolated from P39 cells. M161Ag can be used in the development of a leukaemia treating agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-369470/34.
N-PSDB; AAT75133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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409
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117; Conserv
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                                                                                                                                                                            KERLEQIAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVY
                                                                                                                                                                                                                                                                                            ENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASPLAKKFPSDP
                                                                                                                                                            GEKMNTVINNVLSSTPADVKYNPHVILSVAGPAT--FETVTLPNKGQYVIGVDSDQGMI-
                                                                                                                                                                                                                                                                      AHREELERNQIKIIGIDF-DIETEYKX--FYSLQFNIKESAFTTGYAIASXLSEQ---DE
                                                                                                                                                                                                                                                                                                                          SAFEALKAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIXVLNGFKHQQSIKQY--ID
                                                                                                                                                                                                                                                                                                                                          SGWEAIQQLGALIGGEIISVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIP
| :||::::||:||:|::::|
                                                                                                                                                                                                                                                                                                                                                                              ANNDESNISFKEKDISKYTTTNANGKQVVKNAEL-----LKLKPVLITDEGKIDDKSFNQ
                                                                                                                                                                                                                                                                                                                                                                                                        ADNONKQIT----DVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein M161Ag
IDNVSERLEAIISAIN
                         PDKQQESLDKLITDIN
                                                    --KEKXIGVAENOFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNK
                                                                             GIKDRFVDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQ 405
                                                                                                         -QDKDRILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKXSHFGTQ-----
                                                                                                                                   TKTKNKFFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYL
                                                                                                                                                                                                                  SKRVVASFGGGAFPGVTTFNEGFAKGIPYYNQKH--KSSKIYHTSPVKLDSGF----TA
                                                                                                                                                                                                                                           TKRSAIVIGGGISPAVIDFIAGYLAGIKAWNLKNSDKKTKI-TIDKIEINLGFDVQDTST
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                               17.3%; Score 372; DB 2;
26.8%; Pred. No. 4.8e-21;
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 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development of leukaemia treating
                                                                                                                                                                                                                                                                                                                                                                                                                                    167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
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Search completed: December 18, 2004, 01:22:25
Job time : 112.476 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                       Database :
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Perfect score:
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Issued_Patents_AA:*

1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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1 MWDKETTKEEKSADNQNKQI.....KQPDKQQESLDKLITDINNL 423
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | w | 2 | μ | Result No. |
|-------------------|-------------------|------------------|-------------------|----------|----------------------|--------------------|-----------------|---------------------|-------------------|-------------------|-----------------|------------------|-------------------|---------------------|---------------------|-------------------|------------------|------------------|---------------------|-------------------|-----------------|--------------------|-------------------|-------------------|-------------------|-------------------|-----------------------|
| 119 | 119 | 119.5 | 121.5 | 121.5 | 127.5 | 133 | 133.5 | 136 | 137.5 | 137.5 | 143 | 161 | 173 | 174 | 178 | 178 | 178 | 178 | 202 | 202 | 202 | 204 | 375.5 | 375.5 | 378.5 | 378.5 | Score |
| ٠. ن | | | | | 5.9 | ٠ | • | | 6.4 | | ი. ი | 7.5 | | 8.1 | | | | 8.3 | | 9.4 | | 9.5 | 17.4 | 17.4 | 17.6 | 17.6 | Query Match Length |
| 5822 | 878 | 834 | 1079 | 1073 | 518 | 867 | 1786 | 553 | 889 | 889 | 353 | 339 | 166 | 362 | 375 | 361 | 341 | 339 | 374 | 328 | 328 | 363 | 428 | 404 | 428 | 404 | |
| L | Δ. | 4. | 4 | 4 | 4. | 4. | w | w | 4 | w | W | _ | 4 | 4 | 4 | 4 | ۳ | 4 | 4. | 4 | w | 4 | 4 | 4 | 4 | 4 | 80 |
| US-09-308-375-2 | -09-540-236 | US-09-187-999-11 | -09-206-942 | -09-206- | US-09-248-796A-18238 | US-09-540-236-2676 | US-08-973-462-8 | US-09-134-001C-2974 | US-09-952-267B-15 | US-09-336-447A-15 | US-08-313-412-1 | US-08-396-957A-4 | US-09-182-625F-6 | US-09-134-000C-6004 | US-09-134-000C-6005 | US-09-071-035-78 | US-08-396-957A-5 | US-09-071-035-80 | US-09-107-532A-5084 | US-09-536-784-8 | US-08-961-083-8 | US-09-583-110-2686 | US-09-182-625F-16 | US-09-182-625F-15 | US-09-182-625F-9 | US-09-182-625F-14 | ID |
| Sequence 2, Appli | Sequence 3401, Ap | | Sequence 47, Appl | 49, | Sequence 18238, A | Sequence 2676, Ap | | Sequence 2974, Ap | 15, | 15 | ŗ | 4. | Sequence 6, Appli | Sequence 6004, Ap | 60 | Sequence 78, Appl | ū | 80 | 50 | Sequence 8, Appli | θ, | e 2686 | 16, | 15, | Sequence 9, Appli | Sequence 14, Appl | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 3 5 | 34 | 33 | ა 2 | | 30 | 29 | 0.7 |
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| 112.5 | 113 | 113 | 113 | 113 | 113 | 113 | 113.5 | 115.5 | 116.5 | 117.5 | 117.5 | 117.5 | 117.5 | 117.5 | | 117.5 | FF |
| 5.2 | 5.2 | 5.2 | 5.2 | 5. 2 | 5.2 | 5.2 | ω | 5.4 | 5.4 | ა ა | ა ა | ნ | 5.5 | 5 5 | 5.5 | 5.5 | |
| 1166 | 2777 | 2353 | 2353 | 2353 | 2353 | 2353 | 941 | 5024 | 1104 | 1098 | 1098 | 1098 | 1098 | 1098 | 1098 | 1098 | 1000 |
| 4 | 4 | 4 | 4 | w | w | w | w | 4 | w | 4 | 4 | w | w | w | w | w | ۲ |
| US-09-200-650E-7 | US-09-543-681A-6124 | US-09-684-707-4 | US-09-797-862-33 | US-09-669-974-33 | US-08-913-942-4 | US-09-377-155-33 | US-09-074-658-75 | US-09-710-279-2964 | US-08-923-992A-4 | US-09-684-707-2 | US-09-797-862-32 | US-09-268-347-44 | US-09-669-974-32 | US-08-913-942-2 | US-09-377-155-32 | US-08-685-467-2 | 00 00 100 100 1 |
| Sequence 7, | Sequence 61 | Sequence 4, | Sequence 33, | Sequence 33, | Sequence 4, | Sequence 3: | Sequence 7: | Sequence 29 | Sequence 4 | Sequence 2 | Sequence 32 | Sequence 44 | Sequence 37 | Sequence 2, | Sequence 32, | Sequence 2, | Contraction of |
| 7, Appli | 6124, Ap | 4, Appli | 3, Appl | 3, Appl | , Appli | 3, Appl | 75, Appl | 2964, Ap | , Appli | , Appli | • | 4, Appl | 2, Appl | , Appli | 2, Appl | , Appli | |

ALIGNMENTS

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| γQ | 뮹 | δ | B & | B | Ş | ₽ & | Db | γQ | Db | Ş | Query Match Best Local Matches 11 | US-09-182-62: US-09-182-62: US-09-182-62: US-09-182-62: US-09-182-62: US-09-182-62: US-09-182-62: |
| 354 VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE 411 | : :: : | 304 FFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353 | 254 IASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303 : : | | 195 VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 253 | 135 TEKNIIILGIUWIDTENVIPTEKIINITIKIEBAGWIAGSTAGASTIAKAFFSDETKKSAI 199 | 63 KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQYIDAHREEL 119 | 75 QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134 : : : : : : : : ::: | : : : : : 3 | 31 NERKSETMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWBAI 74 | Query Match 17.6%; Score 378.5; DB 4; Length 404; Best Local Similarity 26.7%; Pred. No. 3.5e-27; Matches 115; Conservative 88; Mismatches 156; Indels 71; Gaps 17; | WS-09-102-625F-14 (US-09-102-625F-14 (Sequence 14, Application US/09102625F Patent No. 6506892 (EARRAL INFORMATION: APPLICANT: Webb, Andrew C. APPLICANT: Blazar, Beverly A. TITLE OF INVENTION: Regulation FILE REFERENCE: BLAZ-101XC1 CURRENT APPLICATION NUMBER: US/09/182,625F CURRENT APPLICATION NUMBER: US/09/182,625F CURRENT FILING DATE: 1908-10-29 PRIOR APPLICATION NUMBER: US 60/063,701 PRIOR FILING DATE: 1997-10-29 NUMBER OF SEQ ID NO: 16 SEQ ID NO 14 LENGTH: 404 TYPE: PRT ORGANISM: Mycoplasma fermentans US-09-182-625F-14 |

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; Sequence 15, Application U
; Patent No. 6506892
; GENERAL INFORMATION:
; APPLICANT: Webb, Andrew C
; APPLICANT: Blazar, Bever
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US-09-182-625F-15
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; TYPE: PRT
; ORGANISM: Mycoplasma
US-09-182-625F-9
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US-09-182-625F-9
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APPLICANT: Blazar, Beverly A.
APPLICANT: Blazar, Beverly A.
TITLE OF INVENTION: Polynucleotides Encoding a Mycoplasma Protein Involved in TITLE OF INVENTION: Regulation
FILE REFERENCE: BLAZ-101XC1
CURRENT PRILICATION NUMBER: US/09/182,625F
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NOS: 16
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Best Local
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26.7%;
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Pred. No. 3.9e-27;
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APPLICANT: Webb, Andrew C.
APPLICANT: Blazar, Beverly A.
APPLICANT: Blazar, Beverly A.
TITLE OF INVENTION: Regulation
FILE REFERENCE: BLAZ-101XC1
CURRENT APPLICATION NUMBER: US/09/182,625F
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR PILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 16
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Sequence 16, Application US/09182625F
Patent No. 6506892
GENERAL INFORMATION:
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                                                 ORGANISM: Mycoplasma
                                                                        TYPE: PRT
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PRIOR FILING LALE.

PRIOR APPLICATION NUMBER: US 60/085,151

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 2686

LENGTH: 363
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US-09-583-110-2686
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; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2686
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Patent No. 66997
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CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pnoumoniae for Diagnostics and Therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
141 ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ERNOIKIIGIDF-DIETEYKW--FYSLOFNIKESAFTTGYAIASWLSEQ---DESKRVVA 197
                                     94 QSTSEADYANNLQQAAGSYNLI------FGVGFALHNAVEEAAKEHTDLNYV 139
                                                                                                                                  38
                                                                                                                                                                         33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNOSGWEAIQQLGA---LTGGEITSVD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
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                                                                                                                                                                                                                   h 9.5%; Score 204; DB 4; Length 363; Similarity 25.7%; Pred. No. 9.8e-11; 98; Conservative 53; Mismatches 147; Indels
                                                                                 SSTAELE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDKLITDIN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPILITDEGKIDDKSFNQSAFEAL 86
                                                                                                                               RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTYF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09583110
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US-08-961-083-8
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Patent No. 6159469
                                                                                                                                                       Matches
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Choi e
                                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: HP Vectra 481
OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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                    90 SSTAELE----
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                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD- 236
                                                                 RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTYF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K----AVEDAKAKILDGSVKVP 361
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                                                                                                                                                                                                                                                                                                                                                                                                                    (301) 309-85
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                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                       9.4%;
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Streptococcus pneumoniae Antigens and Vaccines
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                -GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140
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                                                                                                                                                  ; Score 202; DB 3; I; Pred. No. 1.3e-10; 55; Mismatches 145;
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                                                                                                                                                                                            Length 328;
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-536-784-8
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US-09-536-784-8
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                                                                         Matches
                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: -(Ubknown)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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ADDRESSEE: Human Genome Scientification of the Street Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK 259
33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGEITSVD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                         98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLATEAISEAKKEFEEKTKTIP 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOPTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366
                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                  LENGTH: 328 amino acids
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                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20850
                                                                                                                                                                                                                                                                                                                                                                        (301) 309-8504
                                                                9.4%; Score 202; DB 4; Length 328; 25.7%; Pred. No. 1.3e-10; tive 55; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEGK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4Mb storage
                                                                    84;
                                                                  Gaps
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US-09-107-532A-5084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5084, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5084:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                    MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
        FEATURE:
                                                ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K----AVEDAKAKILDGSVKVP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIDDVIKDOKNV-----ASVTFADNESGYLAGVAAAK----TTKTKQVGFVGGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTABLE-----
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                                                                                                            TOPOLOGY: linear
                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLATEAISEAKKEFEEKTKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STLKQVGTTVKDI-----SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEGK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --IVYQVAGGTGAGVFABAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
                          ORGANISM: Enterococcus
                                                                                                                                                    LENGTH: 374 amino acids
                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Beaver Street
                                                                                                                                                                                                                    (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OUCCETTE-Stamm and David Bush
NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140
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RESULT 9
US-09-071-035-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 80, Application US/09071035
Patent NO. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
           APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brockes
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 98369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                       COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 ADGK-----FPGGEHTVY-GLKEDGVGLTEGQLSDEAKK----AVDEAKEKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 SNSRNLAGFEFGKKSATVYLGIKDRFYDIADTSLEGNDKKLATEAISEAKKEFEEKTKTI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 AKSLNESGDKKVWVIGVDRDQSDEGEYTLNGEKKNFTLTSTLKAVG----TVVEDLAQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 I--IANQNDR--YLIGVDTDQS-----LVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 TFKDNEASYLAGVAAAY-----TTETNVVGFIGGVKGEVIDRFDAGFKAGVDA-GA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 TYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 NIDQALNAGFKTIFGIGYKLKPAIQEQATNNTGTNFVIIDDVIDGLD--NV-----VSA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 KNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIA----SKDKPSTLLAVAGPLTEIFSD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 -----LSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILG--IDWTDTENVIPTGRYINL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ALITDTGGVDDRSFNQSAWEGLEKWGK-----DQGLSRGNDGFQYFQSSNESDYIP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWV- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                             20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                 Diskette,
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(B) LOCATION 1...374
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25.2%;
                                                                                                                                                                                                                                                                                                                                                   MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496
                                                                                                                                                                                                                                                                                                                                                                                              3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 5084:
80:
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US-08-396-957A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08396957A Patent No. 5780041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 103; Conserv
                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,957
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDMBER: 08/020,245
FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: SIMPSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SIMPSON, VITITLE OF INVENTION: ITITLE OF INVENTION: OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
CYPEANTERISTICS:
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 345 PA
CITY: NEW YORK
FILING DATE:
                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKVGFVGGEEG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA-----ISSAADANPDTNFVLI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNOSSWEGLOAWGKEHDLPEGSKGYAY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                       10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK----
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                                                                                                                                                                                                                                                                                                                                                                                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                             345 PARK AVENUE
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                                                                                                                                                                                                                                                                                                         FLOPPY DISK
05-MAY-1991
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                    07/664,731
                                                                                                                                                                                               US/08/396,957A
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APPLICATION NUMBER: 07/4
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:

07/487,716

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US-09-071-035-78
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Sequence 78, Application US/09071035
Patent No. 6448043
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: p39a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DOROTHY R. AUTH REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: D39a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                                                                                                                         209 AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 ANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSS--
                                                                                                                                                                                                                            AAGLAGIGVIEAAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y
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                                                                                                                                                                IKNNNV----WEGGK----VVQMGLRDGVIGLPNAN--
                                                                                                                                                                                            TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 384
                                                                                                                                                                                                                                                                                             YGYESGAKYAN-KDIEIISEYSNSFSDVDIG-----RTIASKMYSKGIDVIHF
                                                                                                                                                                                                                                                                                                                                                                                                                           SDLDNLKRNGSDLIW-LVGYMLTDA--SLLVSSENPKI--SYGIIDPIYGDDVQIPENLI 133
                                                                                                                              KTIPAEEVRKTLEIP 399
                                                                                                                                                                                                                                                            AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY 324
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-071-035-78
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Best Local Similarity 25.1%; Pred. No. 2.8e-08;
Matches 103; Conservative 51; Mismatches 140;
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APPLICANT: Gil H. Choi
TITLE OF INVENTION: En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (:
INFORMATION FOR
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APPLICATION NUMBER:
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ODERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CITY: Rockville
STATE: Maryland
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE-----
                                   VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                      TLLAVAGPLTEIFSDII-----
                                                                                                                                                                                                                             VVIDRFQAGFEKGV-ADAAKELGKEITVDT----
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                                                                                                         KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                               KGKALAAAMYQNGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY-
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                                                                                                                                                                                                                                                                                                                                                                                                                    ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
                                                                          KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK
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(301) 309-8512
FOR SEQ ID NO: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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 -----KEAVKTAKDKVISGDVKVPEKPE
                                                                                                                                                                                    -----ANONDR-YLIGVDTDOSL--VYT
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                                                                          FPGGEHLVY-GLKDGG 326
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   361
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Sequence 6004, Application US/09134000C

PATENT NO. 6617156

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
ITITLE OF INVENTION: NUCLEIC ACID AND AMINO ACI
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOI
FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILLY DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PATENTIN VERSION 3.1
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOLE
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 6005
LENGTH: 375
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US-09-134-000C-6004
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          S
                                                                             SEQ ID NO 6004
LENGTH: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.3%; Score 178; DB 4; Length 375; Best Local Similarity 25.1%; Pred. No. 3e-08;
TYPE: PRT
ORGANISM: Enterococcus faecalis
-09-134-000C-6004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 KGKALAAAMYQNGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 TLLAVAGPLTEIFSDII---------ANQNDR-YLIGVDTDQSL--VYT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKVGFVGGEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 | TSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLK|PENKQLFTEKNIIIL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNQSSWEGLQAWGKEHDLPEGSKGYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVIDREQAGEEKGV-ADAAKELGKEITVDT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA-----ISSAADANPDTNFVLI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Mismatches 140; Indels 116;
                                                                                                                                                                                                                                                                                                          ACID SEQUENCES RELATING
FOR DIAGNOSTICS AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACID SEQUENCES RELATING TO FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 60/063,701
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09182625F
PATENT NO. 6506892
GENERAL INFORMATION:
APPLICANT: Webb, Andrew C.
APPLICANT: Blazar, Beverly A.
APPLICANT: Blazar, Beverly A.
TITLE OF INVENTION: Polynucleotides Encoding
TITLE OF INVENTION: Regulation
FILE REFERENCE: BLAZ-101XC1
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Best Local S
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                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycoplasma fermentans FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 LASTIKGVNIAV-KKISDLALEDK-----FPGGEH---LTYGLKDGGVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 EIFSDII-----KTKNKF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 EKGV-----ADAGKK------LGKDIQITSTYAGTFADASKGR-----ALASSMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 IPTGRYINLTYKTBEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGY 211
                                                                                                                                                                                                               197 GGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 LEGKYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SKKNANTKGDPQH----SVVMVTDTAGIDDKSFNQSAWEGMQEWG--KEHKLPEGPQGYAY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 AKADAN-----KHFGLMMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAE
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96; Conserv
                                                                                                        S------KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFF 305
                                                                                                                                                                      GGGAFPGVTTENEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVI
  TSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ------KEKWIG 162
                                      TSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVD 355
                                                                                    NNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKKLATEAIS-EAKKEFEEKTKTIPAEEVRKTLEIPEMP 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAGADIIYHAAATTGQGIFQEAKALNETGSKDKVWVIGVDRDQNEDGKYTTKDGKDDNLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LTTEALSDOAKTAVKEAKEQIISGDVK----VPDQP 362
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                        8.0%; Score 173; DB 4; Length 166; 27.3%; Pred. No. 2.4e-08; rative 37; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.1%; Score 174; DB 4; Length 362;
24.1%; Pred. No. 6.7e-08;
ative 67; Mismatches 132; Indels 104;
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US-08-396-957A-4
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US-08-396-957A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/396,95:
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,245
FILING DATE: 19-FEB-1993
CLASSIFICATION DATA:
APPLICATION UNBER: 07/664,731
PRIOR APPLICATION NUMBER: 07/664,731
FILING DATE: 05-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 751-68
TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        MOLECULE TYPE: I
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 339
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,434
REPERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SIMPSON, TITLE OF INVENTION:
                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
        NAME/KEY: p39'
LOCATION:
LOCATION METHOD:
LOCATION METHOD:
LOCATION: p39' prot
OTHER INFORMATION: sequence.
                                                                                                                                    CELL TYPE:
                                                                                                                    ORGANELLE:
                                                                                                                                                                        TISSUE TYPE:
                                                                                                                                                                                                        DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                        STRAIN: Sh-2-82 INDIVIDUAL ISOLATE:
                                                                                                                                                                                      HAPLOTYPE:
                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
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STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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| VAE 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (212)
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                                                                                                                                                                                                                                                          Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                              unknown
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                            protein
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ANTIGNIC PROTEINS AND
GENES ENCODING SAME OF BORRELIA BURGDORFERI.
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                                p39' protein
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Best Local Similarity
                                    407
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                                                                                                                                             239
                                                                                                                                                                                   287
                                                                                                                                                                                                                       189 YİGSFADLEAĞRSVATRMYSDEID-----IIHHAAGİGGİGAIEVAKELGSGHYI
                                                                                                                                                                                                                                                                                              143
326 -SNKESYEKFLKE 337
                                                                      286 YGLKEGVVGFV----RNPKMISF-----
                                                                                                                                                                                                                                                        233 KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL 286
                                                                                                                                                                                                                                                                                                                               174 YANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD 232
                                                                                                                                                                                                                                                                                                                                                                                                       115 FQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                           37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85;
                                                                                                                                             xresdvakvaalQnpdmkyai------Idpiysndpip-anlvGmteraQeGaflTG 142
                                  DKQQESLDKLITD 419
                                                                                                         LGIKDRFYDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP 406
                                                                                                                                                                             IGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY 346
                                                                                                                                                                                                                                                                                              YIAAKL-----SKTGKİGFLGGİEGEIVDAFRYGYEAGAKYAN-----KDIKİSTQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEG----LKDAGSDLIWLIG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 68; Mismatches 136; Indels 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 161; DB 1
Pred. No. 1e-06;
                                                                        --ELEKEIDNLSSKIINKEIIVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                       238
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Search completed: December 18, 2004, 01:28:36 Job time: 30.0389 secs

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Title:
Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
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2155
1 MWDKETTKEEKSAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1589859 seqs, 357834939 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd
/cgn2_6/ptodata/2/pubpaa/US09E_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOME.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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Pred. No. is the score greater the and is derived is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

| 112110987654 112110987654 | . w z, p | Result No. |
|---|---|--------------------------|
| 216.5 216.5 213.5 213.5 209 202 202 178 | 220.5 | Score |
| 110000 99999999999999999999999999999999 | 10.0 | Query Match Length DB |
| | 330 | Length- |
| 15 15 15 15 15 15 15 | | B |
| US-10-451-337-39 US-10-451-337-41 US-10-451-337-41 US-10-451-337-16 US-10-451-337-6 US-10-451-337-6 US-09-765-272-8 US-09-765-272-8 US-09-765-272-8 US-09-765-276-80 | US-10-474-792-166 US-10-451-337-12 US-10-451-337-14 | ID |
| Sequence 39, Appl Sequence 41, Appl Sequence 11, Appl Sequence 16, Appl Sequence 6, Appl Sequence 6, Appli Sequence 132, App Sequence 132, App Sequence 80, Appl Sequence 80, Appl | Sequence 166, App Sequence 12, Appl Sequence 14, Appl | Description |

ALIGNMENTS

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Sequence 166, Application US/10474792

Publication No. US20040236072A1

GENERAL INFORMATION:

APPLICANT: Olmsted, Stephen

APPLICANT: Zagursky, Robert

APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

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APPLICANT: Nickbarg, Eliot

APPLICANT: Nickbarg, Eliot

APPLICANT: Nonescape

FILE REFERENCE: AM 100399

CURRENT APPLICATION NUMBER: US/10/474,792

CURRENT APPLICATION NUMBER: 2003-10-14

NUMBER OF SEQ ID NOS: 674

SOPTWARE: Patentin version 3.0

SEQ ID NO 166

LENGTH: 350

TYPE: PRT
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US-10-474-792-166
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
136 DNVASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG 186
                                                         156 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG 214
                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                         86 EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK 135
                                                                                                                                                                                   98 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 155
                                                                                                                                                                                                                                                                               39 AAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTG-GEITSVDSSTAELEG 97
                                                                                                                                                                                                                                            26 ASKGGASGKTDLKVAMVTDTGGVDDKSFNOSAWEGLOSWGKEMGLOKGTGFDYFOSTSES 85
                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 220.5; DB 17; Length 350; ilarity 27.8%; Pred. No. 2.6e-08; Conservative 49; Mismatches 150; Indels 69;
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US-10-451-337-12
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Best Local
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TYPE: PRT
ORGANISM: S. 1
3-10-451-337-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS.
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REPERENCE: 12806-24PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/256,940 PRIOR FILING DATE: 2000-12-21 NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 10.0%; Score 216.5; DB 15; Length 330; Local Similarity 28.3%; Pred. No. 4.7e-08;
                                                                                     226
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                                                                                                                                                                                                                                                        129 DNVASVTFADHEAAYLAGIAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG
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LINKQVADKK-----FPGGK--TTVY-GLKDGGVEIATT----NVSKEAVKAIKEAK
                    SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 377
                                                                                GAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQ 285
                                                                                                                           LTEIFSDIIANQNDR-----YLIGYDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 317
                                                                                                                                                                          VKS---
                                                                                                                                                                                                              IKAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGP
                                                                                                                                                                                                                                                                                                GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG 214
                                                                                                                                                                                                                                                                                                                                           EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK 128
                                                                                                                                                                                                                                                                                                                                                                                   KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 155
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                                                                                                                                                                   -----VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT
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APPLICANT: SHARE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAMEL, Josee
APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, PALTICK
TITLE OF INVENTION: STREEPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
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APPLICANT: RIGUX, Stephane
APPLICANT: RHEAULT, Patrick
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS ANI
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
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APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
APPLICANT: HAWEL, Josee
APPLICANT: RICUX, Stephane
APPLICANT: RHEAULT, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뭐
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/10451337 Publication No. US20040097706A1
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TYPE: PRT
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28.3%;
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Pred. No. 4.7e-08;
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APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: MEDDEUR, Bernard R.
APPLICANT: HAMEL, JOSEE
APPLICANT: RIGUX, Stephane
APPLICANT: RIGUX, Stephane
APPLICANT: RIGUX, Stephane
APPLICANT: RIGUX, STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT APPLICATION NUMBER: US 60/256,940
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
NUMBER: DESCE 65.
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; SOFTMARE: FABLSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 330
; TYPE: PRT
; ORGANISM: S. pyogenes
US-10-451-337-39
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                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: S. pyogenes
US-10-451-337-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/10451337 Publication No. US20040097706A1
                                                                                                                                           Query Match 10.0%; Score 216.5; DB 15; Length 330; Best Local Similarity 28.3%; Pred. No. 4.7e-08; Matches 102; Conservative 46; Mismatches 143; Indels 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.0%; Score 216.5; DB 15; Length 330; Best Local Similarity 28.3%; Pred. No. 4.7e-08; Matches 102; Conservative 46; Mismatches 143; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF 317
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98 KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 155
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                                                              ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSES 78
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US-10-451-337-41
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CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 330
TYPE: ERT
ORGANISM: S. pyogenes
US-10-451-337-41
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Publication No. US20040097706A1
GENERAL INFORMATION:
APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
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Best Local Similarity
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APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
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-FPGGK--TTVY-GLKDGGVEIATT----
   -NVSKEAVKAIKEAK
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RESULT 8
US-10-451-337-42
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US-10-451-337-16
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US-10-451-337-16
                                                                                                                                                                                                                                                                                  Sequence 42, Application US/10451337 Publication No. US20040097706A1 GENERAL INFORMATION:
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Best Local S
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CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
                                                                   APPLICANT: HAMEL, JOSEE
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPFOCOCCUS PYOGENES ANTIGENS
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
                                                                                                                                                                                                                                    APPLICANT: SHIRE BIOCHEM INC. APPLICANT: MARTIN, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 12806-24PCT CURRENT APPLICATION NUMBER: US/10/451,337 CURRENT FILING DATE: 2003-11-18 PRIOR APPLICATION NUMBER: US 60/256,940 PRIOR FILING DATE: 2000-12-21 NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
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APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard
APPLICANT: HAMEL, Josee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 VKS-----VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                             286 LINKQVADKK-----FPGGK--TTVY-GLKDGGVEIATT----NVSKEAVKAIKEAK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNVASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYSSLANTNKNVWVLSGFQ--HGDAFTRWLKIPENKQLFTEKNIIILGIDWIDTENVIPT 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQ 285
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BRODEUR, Bernard R.
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RIOUX, Stephane
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; LENGTH: 344
; TYPE: PRT
; ORGANISM: S. ]
US-10-451-337-6
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; ORGANISM: Mouse
US-10-451-337-42
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US-10-451-337-6
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NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 42
                                                                                                                         Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10451337
Publication No. US20040097706A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HAMEL, Josee
APPLICANT: RIOUX, Stephane
APPLICANT: RHEAULT, Patrick
TITLE OF INVENTION: STREPTOCOCCUS PYOGENES ANTIGENS AND
TITLE OF INVENTION: CORRESPONDING DNA FRAGMENTS
FILE REFERENCE: 12806-24PCT
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/451,337
CURRENT FILLIG DATE: 2003-11-18
PRIOR APPLICATION NUMBER: US 60/256,940
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHIRE BIOCHEM INC.
APPLICANT: MARTIN, Denis
APPLICANT: BRODEUR, Bernard R.
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                                         ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGQSWGKEMGLQKG---TGFDYFQSTS 81
                                                                                AAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAI---QQLGALTGGEITSVDSSTAEL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK 377
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EGKYSSLANTNKNVWVLSGFQ--HGDAFTRWLK-----IPENKQLFTEKNIIILGIDWT 147
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                                                                                                                       9.7%; Score 209; DB 15;
27.9%; Pred. No. 1.9e-07;
ative 48; Mismatches 138;
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                                                                                                                             Indels 86;
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| Qy 33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVD 89 | Query Match 9.4%; Score 202; DB 9; Length 328; Best Local Similarity 25.7%; Pred. No. 5.9e-07; Matches 98; Conservative 55; Mismatches 145; Indels 84; Gaps 19; | SEQUENCE CHARACTERISTICS: LENGTH: 328 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-765-272-8 | NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB340P2 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 8: | CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/765,272 APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001 CLASSIFICATION: <unknown> PRIOR APPLICATION NUMBER: 08/961,083 FILING DATE: <unknown> ATTONNEY/AGENT INCOMPANTION.</unknown></unknown> | CITY: Rockville STATE: Maryland COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 COMPUTER: MSDOS version 6.2 | RESULT 10 US-09-765-272-8 ; Sequence 8, Application US/09765272 ; Patent No. US20020061545A1 ; GENERAL INFORMATION: TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines ; NUMBER OF SEQUENCES: 452 ; CORRESPONDENCE ADDRESS: ADDRESSEET: 9410 Key West Avenue | Oy 372 AISEAKKEFEEKTKTIP 388 : : Db 326 AIKEAKAKIKSGDIKVP 342 | Db 222 YQAAGGTGAGVFNEAAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKE 281 Qy 312 LGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATE 371 | Db 134NVASVTFADHEAAYLAGIAAAKTTKTKTVGFVGGMEGTVITR 175 Qy 208 IAGYLAGIKAMNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPST 262 Qy | : : : |
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| Qy 260 PSTLLAVAGPL-TEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFT 306 | OY 201 -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVODTSTKERLEQIASKDK 259 | QY 90 SSTAELE | Query Match 9.4%; Score 202; DB 10; Length 350; Best Local Similarity 25.7%; Pred. No. 6.4e-07; Matches 98; Conservative 55; Mismatches 145; Indels 84; Gaps 19; Qy 33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQOLGALTGGEITSVD 89 | NUMBER OF SEQ ID NOS: 388 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 132 LENGTH: 350 TYPE: PRT ORGANISM: Streptococcus pneumoniae US-09-769-787-132 | ; APPLICANT: HANSDYO, PHILLD M ; TITLE OF INVENTION: PYCCHING ; FILE REFERENCE: PWC/P21129WO ; CURRENT FILING NOWBER: US/09/769,787 ; CURRENT FILING DATE: 2001-01-26 ; CURRENT FILING DATE: 1998-03-71 ; PRIOR APPLICATION NUMBER: GB 9816337.1 ; PRIOR FILING DATE: 1998-03-27 ; PRIOR APPLICATION NUMBER: US 60/125164 ; PRIOR FILING DATE: 1998-03-19 | 9 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 | QY 307 SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366 | Db 150 ESEVISRPEAGFKAGVASVDPSIKVQVDYAG-SEG-DAKGKTIAAAQYAAGAD- 201 Qy 260 PSTLLAVAGPL-TEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFT 306 | OD STSEADYANNLQQAAGSYNLIFGVGFALNNAVKJJAAKEHIJUHNIV 104 QY 141 ILGIDWIDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI 200 | : |

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US-09-071-035-80
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Publication No.
                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                        Best Local Similarity
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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203 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS 261
                                                       113 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKVGFVGGEEG 157
                                                                                       143 GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 202
                                                                                                                                                                                                                                                                        103;
                                                                                                                              63
                                                                                                                                                                                                                                  33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNOSGWEAIOOLGA---LTGGE----
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                                                                                                                                                          ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
                                                                                                                                                                                               KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNOSSWEGLOAWGKEHDLPEGSKGYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K----AVEDAKAKILDGSVKVP 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLKQVGTTVKDI-----SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEGK 330
                                                                                                                          IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA----ISSAADANPDTNFVLI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09071035
                                                                                                                                                                                                                                                                                                                                                                                                                                339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                    8.3%; Score 178; DB 9; Length 33: ilarity 25.1%; Pred. No. 4e-05; Conservative 51; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309-8512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/071,035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PB369P2
                                                                                                                                                                                                                                                                                                     DB 9; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              storage
                                                                                                                                                                                                                                                                      116;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                 62
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TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-206-576-80
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US-10-206-576-80
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                                                                                                                                                         Matches 103;
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Choi et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-U1-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
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63
                                                                                                                33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLLAVAGPLTEIFSDII-----
                                  ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
                                                                         KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNQSSWEGLQAWGKEHDLPEGSKGYAY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDLTDGYL--NDKT------KEAVKTAKDKVISGDVKVPEKPE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK----
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IQSNDAADYTTNIDQAVSSKFNTIFGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Dell Latitude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human
                                                                                                                                                                                                                                                                                                                                                       ENGTH: 339 amino acids
                                                                                                                                                         Conservative
                                                                                                                                                                           8.3%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sciences, Inc
                                                                                                                                                         51; Mismatches 140;
                                                                                                                                                                           Score 178; DB 1
Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                   PB369P1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                           80:
    -GYLLKDA---
                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ANQNDR-YLIGVDTDQSL--VYT 298
                                                                                                                                                                                            Length 339;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --FPGGEHLVY-GLKDGG 304
    -ISSAADANPDTNFVLI 112
                                                                                                                                                           116;
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                                                                                                                                                         Gaps
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: F
US-09-071-035-78
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US-09-071-035-78
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                                                                                                           Query Match
                                                                                                                                                                                                                                          TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gil H.
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                           Local
                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK-----FPGGEHLVY-GLKDGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 KGKALAAAMYONGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 DDQIDGKKNV-----VSATFRDNEAAYLAGVAAA-----NETKTNKVGFVGGEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
                       33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20850
                                                                                       Similarity
KTAESGGGKGDA----AHSAVIITDTGGVDDKSFNQSSWEGLQAWGKEHDLPEGSKGYAY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gil H. Choi
                                                                   8.3%; Score 178; DB 9; Length 361; larity 25.1%; Pred. No. 4.4e-05; Conservative 51; Mismatches 140; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u: Diskette, 3.50 inch, 1.4Mb storage
HP Vectra 486/33
                                                                                                                                                                                        linear
                                                                                                                                                                    protein
                                                                                                                                                                                                        single
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RESULT 15
US-10-206-576-78
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                                                                                                                               INFORMATION FOR SEQ ID NO: 78: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/071,035

FILING DATE: 1998-05-04

APPLICATION NUMBER: US 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: US 60/044,031

FILING DATE: 1997-05-06

APPLICATION NUMBER: US 60/066,009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-U11-2002
CLASSIFICATION: Unknown>
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGKALAAAMYQNGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDQIDGKKNV-----VSATFRDNÉAAYLAGVAAA-----NETKTNKVGFVGGEEG 179
                                                               STRANDEDNESS: single
                                                                                      TYPE: amino acid
                                                                                                                                                                                              NAME: Hyman, Mark J. REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Dell Latitude OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 Key West
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDLTDGYL--NDKT------KEAVKTAKDKVISGDVKVPEKPE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQSNDAADYTTNIDQAVSSKFNTIFGI----GYLLKDA----ISSAADANPDTNFVLI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITSVDSS--TABLEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PB369P1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                          LENGTH: 361 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20850
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    78:
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Query Match

8.3%;

Score 178;

DB 14;

Length 361;

| Search com | Db | 8 | В | 8 | DЬ | 8 | Db | Ş | Db | Qy | В | 8 | В | ş | Best Loc Matches |
|---|---|--|--|---|--|--|------------------------------------|--|---|--|---|---|--|--|---|
| Search completed: December 18, 2004, 01:44:03 | 327 VDLTDGYLNDKTKEAVKTAKDKVISGDVKVPEKPE 361 | 354 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403 | 278 KTKDGKEDNFTLTSTLKGVGTAVQDIANRALEDKFPGGEHLVY-GLKDGG 326 | 299 KTKNKFETSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353 | 219 KGKALAAAMYQNGVDIIFHASGATGQGVFQEAKDLNESGSGDKVWVIGVDRDQDADGKY- 277 | 262 TLLAVAGPLTEIFSDIIANQNDR-YLIGVDTDQSLVYT 298 | 180 VVIDREQAGFEKGV-ADAAKELGKEITVDT | 203 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIBINLGFDVQDTSTKERLEQIASKDKPS 261 | 135 DDQIDGKKNVVSATFRDNEAAYLAGVAAANETKTNKVGFVGGEEG 179 | 143 GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP 202 | 85 IQSNDAADYTTNIDQAVSSKENTIFGIGYLLKDAISSAADANPDTNFVLI 134 | 85 ITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142 | 29 KTAESGGGKGDAAHSAVIITDTGGVDDKSFNQSSWEGLQAWGKEHDLPEGSKGYAY 84 | 33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGE 84 | Best Local Similarity 25.1%; Pred. No. 4.4e-05; Matches 103; Conservative 51; Mismatches 140; Indels 116; Gaps 20; |

Search completed: December 18, 2004, 01:44:03 Job time: 98.7643 secs

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Title:
Perfect score:
                                                                  Database :
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PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1586.669 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | | | 12 | • | 10 | 9 | œ | 7 | o | ហ | 4 | ω | N | μ | Result |
|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------|----------------|
| 125.5 | 125.5 | 126 | 128 | 131.5 | 132 | 134 | 136 | 139.5 | 139.5 | 140 | 146 | 150 | 152.5 | 161 | 162.5 | 165.5 | 168 | 168.5 | 173 | 177 | 178.5 | 180.5 | 181 | 192 | 198 | 202 | 203.5 | 552 | Score |
| 5. 8 | 5.8 | 5.8 | 5.9 | 6.1 | 6.1 | | | 6.5 | | | | | | | 7 | 7 | 7 | 7 | 8 | 8.2 | 8.3 | 8.4 | 8.4 | ٠ | 9.2 | • | 9.4 | 25.6 | Query Match |
| 1223 | 763 | 349 | 657 | 1558 | 326 | 539 | 547 | 337 | 337 | 379 | 353 | 524 | 591 | 339 | 525 | 360 | 357 | 516 | 357 | 341 | 359 | 350 | 353 | 357 | 374 | 350 | 350 | 461 | Length |
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| E88451 | A82863 | F84246 | S73428 | B71603 | G95857 | D82886 | E29504 | B97374 | AH2591 | H75318 | G70147 | D82944 | D64204 | F70147 | C82914 | H70147 | AD1248 | C82946 | AH1610 | E70147 | F72418 | C70009 | H71340 | D96986 | C97965 | G95097 | F86804 | G | ID |
| | hypothetical prote | hypothetical prote | probable lipoprote | RESA-H3 antigen PF | hypothetical prote | conserved hypothet | mercury(II) reduct | | membrane lipoprote | membrane lipoprote | basic membrane pro | hypothetical membr | membrane lipoprote | basic membrane pro | conserved hypothet | basic membrane pro | CD4+ T cell-stimul | hypothetical prote | Ē | basic membrane lip | basic membrane pro | ABC transporter (1 | membrane lipoprote | probable lipoprote | conserved hypothet | lipoprotein [impor | basic membrane pro | Ř | Description |

ALIGNMENTS

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90555 RESULT 1

B90555
ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain UAB (C;Species: Mycoplasma pulmonis
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C; Genetics:
A; Gene: MYPU 3460
A; Genetic code: SGC3 A;Molecule type: DNA A;Residues: 1-461 <KUR> A;Cross-references: UNIPROT:Q98QL5; GB:AL445566; PID:g14089760; PIDN:CAC13519.1; GSPDB:GN A;Experimental source: strain UAB CTIP 밁 S Ś 밁 Ś 밁 Ş 밁 á 밁 5 밁 ş A; Status: preliminary Query Match Best Local Similarity 322 263 203 167 382 225 143 108 NVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIILLGIDWTDTEN-VIPTGRVINLTYKTE 166 tch 25.6%; Score 552; DB 2; Length 46 al Similarity 31.2%; Pred. No. 1.5e-26; 133; Conservative 82; Mismatches 161; Indels 83 62 NDNSFNQSGWEAIQQLGALTGGEITS------VDSSTAELEGKYSSLANTNK 107 28 AQNPNKTNSNLDSSKITDLLSQKEVTETQKIVENKIKQASLETQK-----VVLITADGNI 13 ADNONKQIT--DVSKISGLVNER------KSEIMAAKADANKHFGLNMAIVTAGGTV NDRYLIGVDTDQSLVYTKTKNKFFTSILKNIGYSVFSVLSDLYT-----KKSNSRNL 333 EAGWQAGYASADFLGTKYANNEAKRAISAFGGGDFAGVTDFLNGFFEGIRAWNSEAENAN 262 EAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWN--LKNSD 224 TWILTGFQQGNEIENFLNDENNLRRFKENKVKIIGVDWAPNANSKIPQGSLISLLFKTE 202 DDKSFNQQVYESQKTLKDFVDKAYKSQNKEAENQHKLDNYINSAVKDLEQNYKVALDRGY 142 GS---NPKNLVLKRGLSAKFVNITKSRVKESIKTQADTSIQKAIDKWNANPNSKKIEKEM KKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII---ANQ 281 AGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEA--KKEFEEKTKTIPAEE 391 EDRFIVGVDTDOSLSFTNDSKRFFTSIVKNIAFPVYQILLALLTKDEESVILKEGNDKFL KKVKIVSENLVLDTGF-IPNAEKNEVVSNVVETGKSTISLPVÅGFFTGVVVDVLRKDTSD 321 Length 461; 50; Gaps 438 82

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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heicon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95097
                                                                                                                                                                                                                                lipoprotein [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change C;Accession: G95097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-350 <STO>
A;Residues: 1-350 <STO>
A;Cross-references: UNIPROT:Q9CFM9; GB:AE005176; PID:g12724428; PIDN:AAK05536.1;
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: bmpA
A; Molecule
  A;Status: preliminary A;Molecule type: DNA
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A88625; MUID:21235186; PMID:11337471
A;Accession: F86804
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEIK-----DAVAKAKADIIDGKITVPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IASKDKPSTLLAVAGPL-TEIFSDIIA-----NQNDR-YLIGVDTDQSLV--YT----KT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LASVAVLAGCRSHDAAGSGKAKTD-----LKAAIVTEIGGVNDRSFNQSAWEGLQSWGK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNEVLYSTIKEVG----NVVKDIADKTKDGKFPGGTIVTYDLKNGGVNLGL----DSAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFIGGMQSDVITRFEKGYEAGAKSVN------PDIKVDVQYAGSFSDAAKGKTIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIBINLGFDVQDTSTKERLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSLEGNDKKLATEAISEAKKEFEEKTKTIPAE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMYGAGDDVVYQCAGGVGTGVFSEAKALNSTKNEADKVWVIGVDQDQEYLGKYKSKDGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITDVSKISGLVNERKSBIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA 79
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; Pred. No. 2.7e-05;
63; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis subsp. lactis (strain
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A;Cross-references: UNIPROT:Q8DQC2; GB:AE007317; PIDN:AAK99551.1; PID:g15458340; GSPDB:C;Genetics:
A;Gene: spr0747
                                                                                                                                                                                                                                                                                                                                   R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C97965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein spr0747 [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: C97965
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A;Cross-references: UNIPROT:Q97RHO;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0845
C;Superfamily: ABC transporter yufN
                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <KUR>
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Matches 97
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                                                                          49
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                                                                                                                                                                   Similarity
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 QSTSEADYANNLQQAAGSYNLI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGEITSVD
                                                                        RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFDQSAWEGLQAWGKEHNLSKDNGFTYF
                                                                                                           RKSEIMAAKADANKHEGLNMAIVTAGGTVNDNSFNOSGWEAIQQLGA---LTGGEITSVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSTLLAVAGPL-TBIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGGI
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                                     GKYSSLANTNKNVWVLSGFOHGDAFTRWLKIPENKOLFTEKNII 140
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Pred. No. 3.3e-05;
                                                                                                                                                  Score 198; DB 2;
Pred. No. 6.4e-05;
4; Mismatches 147
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-- FGVGFALHNAVEEVAKEHTDLNYV
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C.
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D96986
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <KUR>
A;Cross-references: UNIPROT:Q97L60; GB:AE001437; PIDN:AAK78679.1; PID:g15023581; GSPDB:(Genetics: A;Gene: CAC0702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNDKKLATEAISEAKK------EFEEKTKTIPAEEVR 393
                                                                                                                                                                           KFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLE 362
                                                                                                                                                                                                                              GKÉVATSLYNGGCDIVYHÁAGGAGIGVÉ-DVAKSLRDQGKDVWAÍGVDKDQAAGLEKYAD
                                                                                                                                                                                                                                                                              -KERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQNDR----YLIGVDTDQSLVYTKTKN
                                                                                                                                                                                                                                                                                                                                   TKTNKIGFVGGKDQPLINKFLSGYIAGAKTVN-----PNITVEK---NYTNDYSDTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKEYSVDYKAIESKKKDDYQPNLQSLIDNDSDLVFGVGYQMADDLATIAKKYPDKKFAII 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366
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                             --NKHVPSEVLSLVDKYKKAIIDGKIVVPDTVDKAQTFKTDQIK 357
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Infect. Immun. 59, 3536-3546, 1991
A; Fitle: Characterization of the 35-kilodalton Treponema pallidum subsp. pallidum A; Reference number: A43595; MUID:91372962; PMID:1894360
A; Accession: A43595
A, Accession: A43595
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A; Residues: 1-10,'A',12-158,'R',160-353 <SCH>
A; Residues: 1-10,'A',12-158,'R',160-353 <SCH>
A; Cross-references: GB:X57836; NID:g48838; PIDN:CAA40968.1;
A; Note: this protein is shown to incorporate palmitic acid C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: tmpC; TP0319
A;Start codon: GTG
A;Start codon: GTG
C;Superfamily: ABC transporter yufN
C;Superfamily: ABC transporter yufN
C;Keywords: blocked amino end; lipoprotein; membrane protein; thiolester bon
C;Keywords: signal sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <MAT>
F;21-353/Product: membrane lipoprotein tmpC #status predicted <MAT>
F;21-Modified site: fatty acylated amino end (Cys) (in mature form) #status
F;21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane lipoprotein TmpC precursor - syphilis spirochete (Species: Treponema pallidum subsp. pallidum (syphilis spirochete) (C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete) (C; Date: 07-Aug-1998 #sequence revision 07-Aug-1998 #text_change 09-Jul-2004 (C; Dates on: H71340; A4359; S29561 R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, reson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, I.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 37-388, 1998 A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A; Reference number: A71250; MUID:98332770; PMID:9665876
RESULT
C70009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST-AELEGKYSSLANTNKNVW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGMVTDSGDIDDKSFNQQVWEGISRFAQENNAKCKYVTASTDAEYVPSLSAFADENMGLV
                                                                                                                                                        EIP 399
                                                                                                                                                                                                                                                      EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL
                                                                                                                                                                                                                                                                                                        LNGQDVWVIGVDRDQYMDGVYDGSKSVVLTSMVKRA-
                                                                                                                                                                                                                                                                                                                                                         ANQNDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                                                                                                                                                                                                                                              ----PDIQVVVEVANTFSDPQKGQALAAKLYDSGVNVIFQVAGGTGNGVIKEARDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG-----PLTEIFSDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVGVA-AALKAKE-----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD------
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                                                                                                                                                                                                        ----GOSIMFGLEDKAVGIPE-----ENPNLSSAVMEKIRSFEEKI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 181; DB 1;
Pred. No. 0.00065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 353
                                                                                                                                                                                                                                                                                                           ---DVAAERISKMAYDGSFPG-
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R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

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Nature 390, C.R.; Henaut, A.; Hilbert, H.; Pujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y., M.; Ogawar, A.; Odiwara, A.; Odega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yasumoto, K.; Yata, K.; Yoshida, K., A; Atthors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A; Aither The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: C70009
A; Accession: C70009
                                                                                                           basic membrane protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72418
Nature
                                                                               R;Nelson,
                           Garrett, M.M.;
C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
;Accession: C70009
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                                                                               K.E.; Clayton,
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                                                                                                                                                                                                                                                                                                                                                       -KAVDKWKKKIIDGLEIPATEKELKTFKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K----KVDTVVEDV-TKKASDGKFPGGE----TLTYGLDQDGVGISPSKQNLSDDVI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGACGNSEKSSGSGEGKNKFSVAMVTDVGGVDDKSFNQSAWEGIQAFGKENGLKKGKNG
                                                    Stewart, A.M.;
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                                             R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                              --EEKTKTIPAE
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Pred. No. 0.00069;
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Best Local
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                                                                                                                                                                                                                                                                                                                  NVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGIS-PAVTDFIA 209
                                                                                                                                                                                                                                                                                                                                                                                     TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDS-S
                                    ISE---AKKEFEEKTKTIP-AEEVRKTLEIPEM 401
                                                                     DVASYYGVVWAYE---
                                                                                                       GYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEA
                                                                                                                                        IEAAREKFSA-LAGSDKLVDLIDYYTTNGKGFFAIGVDMDQDYM---APGAVLTSAMKRV
                                                                                                                                                                       --ASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNL
                                                                                                                                                                                                            GYEAGIKTYSVLHK-KNVKILRGYTQDFEDPKKGKDLAMSQFAEGADIVFHASGACGNGV
                                                                                                                                                                                                                                              GYLAGIKAWNLKNSDKKTKI----TTDKIEINLGFDVQDTSTKERLEQI-------
                                                                                                                                                                                                                                                                                                                                                   QSDYIPNLSKAAEEADLVFAVGFMMTNDLFKVAKQYPDT--
                                                                                                                                                                                                                                                                                                                                                                                                                      RKFLVISLMIFAVALFGFKVIMVTDVGGLGDKSFNDGTWAGIKQAAEELGIEAKVIQSYE
IAELLYLEKLMKEGTLKVPETQEELDAFEVPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%;
                                                                     -----GTFEGGHR----VLGISEDAVGI--SPMKYTKGLVPNRV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE001696; GB:AE000512; NID:G4980582; PIDN:AAD35196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                      ----YFVGIDITPPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                          276
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                                                                                                                                                                                                                                                                                                                                                      112
                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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RESULT 9

E70147

Basic membrane lipoprotein B (bmpB) - Lyme disease spirochete

C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Bate: 13-Feb-1998 #sequence revision 13-Feb-1998 #text_change 09-Jul-2004
C;Date: 13-Feb-1998 #sequence revision 13-Feb-1998 #text_change 09-Jul-2004
C;Dacession: E70147; 140290; 140242
C;Accession: E70147; 140290; 140242
C;Accession: C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
R;Fraser, C.M.; Casjens, R.; White, R.; A;Molecule type: DNA A;Residues: 1-232,'A',234-317,'V',319-341 <F A;Cross-references: GB:L24194; NID:g508420; R;Simpson, W.J.; Cieplak, W. FEMS Microbiol. Lett. 119, 381-388, 1994 A;Title: Nucloetide sequence and analysis of the A;Reference number: I40289; MUID:94327086; PMID:8 A; Cross-references: UNIPROT: Q45011;
A; Experimental source: strain B31 Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403885
A;Accession: E70147 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzbe; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Nature 390, 580-586, 1997 A; Accession: A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: A; Molecule type: DNA A;Status: preliminary; nucleic acid sequence not shown; translation 1-341 <KLE> GB:AE001143; GB:AE000783; <RES> PMID:8050720 PIDN: AAA72407.1; ĺ'n Borrelia burgdorferi encoding Borrelia PID:g508422 NID:g2688279; PIDN:AAC66758 Roberts, burgdorferi not Hatch,

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243 163

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RESULT 10
AH1610
CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria innocua (strain cCP4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria innocua (strain cCP4cels: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1610
C;Accession: AH1610
R;Glaces; P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blo
R;Glacer, P.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                   A;Accession: AH1610
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPROT:Q92BW7; GB:AL592022; PIDN:CAC96656.1; PID:g16413898; GSPDB:A;Experimental source: strain Clip11262
C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-44,'A',46-179 <RE2>
A;Cross_references: GB:J35050; NID:g516591; PIDN:AAC41402.1; PID:g551744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G Microbiology 140, 2931-2940, 1994
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Best Local S
Matches 101
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Best Local Similarity 26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI
                                                                 101; Conservative
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                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 384
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                                                                                         8.0%; Score 173; DB 2;
24.2%; Pred. No. 0.0021;
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                                                              61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 177; DB 2; Length 341; Pred. No. 0.0011; Indels 124; Indels
                                                                 138;
                                                                                                                        Length 357;
                                                              Indels 118;
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                                                              Gaps
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Voss, H.; Wehland,
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                                                                 23;
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; Feihi, H.
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A;Gene: UU012
A;Genetic code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein UU012 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82946 C;Accession: C82946 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, Pebruary 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views A;Reference number: A82870 A;Accession: C82946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-516 <GLA>
A;Cross-references: GB:AE002100; GB:AF222894; NID:g6898946; PIDN:AAF30417.1; GSPDB:GN001;
A;Experimental source: serovar 3; biovar 1
C;Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 ANDFAKADKGQQİASSMYSSGVDVIFHAAGĞTGNGVFAE-AKNLKKKDPSRAVWVİĞVDR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 -IPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 TNKNVWVLSGFQHGDAFTRWLKIPENKQ--LFTEK---NIIIL---GIDWTDTENVIPTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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L---KNLGYSVFSVLS--DLYTKKSNSRNLAGFEFGKKSATVYLGI----KDRF---VDI
                                                                                                                                                                                                                                                                                                                                                                                          --RYINLTYKTEEAGWLAGYANASFLAKK---FPSDPTKRSAIVIGG--GISPA-VTDFI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGLNMAIVTAGGTVNDNSFNOSG--WEAIQQLGALTGGEITSVDSSTAE-LEGKYSSLAN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DTSTKERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR------YLIGVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKPKNQFAIVDDTI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KANDMEKGTDGYNYLOSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALT----GGEITSVDSSTAELEGKYSSLANTNKNVWVLS------GFQHGDAFTRWLK 126
                                                                    ITKG-ADLILPVAIPQVGIAVTEAIATTSHNVGVIGVDVEIENDQAI--NKKTDKFINTH
                                                                                                                            ASKDKPSTLLAVAGPLTEI-FSDIIANQNDRY-LIGVD----TDQSLVYTKTKNKFFTSI 308
                                                                                                                                                                                                                                                              AGYLAGIKAWNLKNSDKKTK---ITTDKIEINL-----GFDVQDTSTKERLEQI 254
                                                                                                                                                                                                                                                                                                                                   ADRVADVYFKVDEAAFLGGIAAAYMLNSNQAVFGAD----NKLTWGGYVGINAKNTTNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGKRALLMPGYQH-----PERLQNALVNDKFDPNLIALILDGVYNNDNKAEFYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FALGTIITVATSCTQKSTLNYSQFYW-----TSPTSDDDEGFQTKYKSMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQ-----SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSAT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TTKTNKVGFVGGVKGAVIDRFEAGFTAGVKA------VNPNAQIDVQY 205
                                                                                                                                                                                             AGFDLGVKWANEKLKDKNIKQEGTQETKKWINVEQVYASESSAGGFQSDSANAKKIIQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQWDEGKVTANDGKDYNVTLTSEIKRVDIAV----DDLAT----RTKAGDPPGGTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 168.5; DB 2; ilarity .25.1%; Pred. No. 0.0066; Conservative 65; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----
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516; 97;

Gaps

285

228

168

112

62

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A; Attoessant,
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-357 <GLA>
A; Residues: 1-357 <GLA>
A; Cross-references: UNIFROT: Q48754;
A; Cross-references: UNIFROT: Q48754;
                                         RESULT
H70147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
 C; Species: Borr
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AD1248
CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Date: 27-Nov-2001
C; Accession: AD1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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                                                           13
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 cane protein D (bmpD)
Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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                                                                                                                     DAVGLSE----
                                                                                                                                                                                                                                                                      DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK
                                                                                                                                                                                                                                                                                                                                                                                   AIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ----DTSTK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYLDVKKET-DNEASLLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGNLSDGVVGISPSAYHYVIDAFNLAQTNQSDKVSTYDELVNKITNDDLFKTLDKKPVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADTSLEG---
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                                                                                                                                                       RFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP 402
                                                                                                                                                                                            VTANDGKDYNVTLTSEIKRVDIAV----EDLAT-----RAKAGDFPGGTK---IEYGLDK 319
                                                                                                                                                                                                                                -SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD 351
                                                                                                                                                                                                                                                                                                        ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDTDQ-----
                                                                                                                                                                                                                                                                                                                                                KVGFVGGVKGTVIDRFEAGFTAGVKA------VNPNAQIDVQYANDFAKA
                                                                                                                                                                                                                                                                                                                                                                                                                           AIVDDTI-----DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----TTKTN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK-IPENKQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILGACGSSSDDKKSSDDKSSKDF--TVAMVTDTGGVDDRSFNQSAWEGLQKFGKANDMEK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOPDKOQESLDKLITDINN
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23.8%;
                                                                                                                 --HODNISKDVLAKVE---EYKOKIVDGD----IKVPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        %; Score 168; DB 2; Length 357;
%; Pred. No. 0.0042;
62; Mismatches 145; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
homolog - Lyme
(Lyme disease :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422
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ne disease sp
spirochete)
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Dussurget, O.; Entian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #text_change
                   spirochete
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                                                                                                                   357
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tian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maitournam, A.; M
Voss, H.; Wehland
                                                                                                                                                                                                                                                                      271
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Fsihi, H.
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72

YASKIQDGARMLGLISFRHKNPISKYFNSPKDNQ----QVSAVLI-----DEIYDLQTGKD YSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTG-- 156

123

Matches Query Match

Similarity

7.5%;

Conservative

63;

Score 162.5; DB Pred. No. 0.016; 3; Mismatches 13

2

Length

525; 119;

Indels

Gaps

99

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A;Molecule type: DNA
A;Residues: 1-525 <GLA>
A;Cross-references: GB.AB002123; GB:AF222894; NID:g6899229;
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                          C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision
C;Accession: C82914
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 (;Accession: H70147 (C;Accession: C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, M.; Vugt, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
                                                                                                                                                                                        A;Description: The complete sequence A;Reference number: A82870 A;Accession: C82914
                                                                                                                                                                                                                                                           R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical membrane lipoprotein UU226 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealvticum
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A;Genetic code:
                        A;Gene: UU226
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                                            ;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSRNLAGFEFGKKSATVYLGIK-DRFVDIADTSLEGNDKKLATEAI 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LETGV--LDGGK---TMFLGLKEDGLGLVLNENLKSNYSEIYNKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKYAN----SNIKVVSQYVGTFGDFGLG----RSTASNM----YRDGVDIIFAAAG-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKYSSLANTNKN-VWVLSGFOHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 155
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                                                                                                                                                                                                                                                                                                        174 YANASFLAKKEPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD 232
                                                                 286 YGLKEGVVGFV-----RNPKMISF------ELEKEIDNLSSKIINKEIIVP------ 325
                                                                                               347 LGIKDRFYDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP 406
                                                                                                                                      287 IGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY 346
                                                                                                                                                                                                       189 YIGSFADLEAGRSVATRMYSDEID-----IIHHAAGLGGIGAIEVAKELGSGHYI 238
                                                                                                                                                                                                                          233 KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTBIFSDIIANQ--NDRYL 286
                                                                                                                                                                                                                                                                                                                                                                      115 FQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAG 173
326 -SNKESYEKFLKE 337
                               407 DKQQESLDKLITD 419
                                                                                                                                                                                                                                                                                                                                          93 YRFSDVAKVAALQNEDMKYAI------IDPIYSNDPIP-ANLVGMTFRAQEGAFLTG 142
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: Perfect score: US-09-676-249D-4 2155 1 MWDKETTKEEKSADNQNKQI......KQPDKQQESLDKLITDINNL 423

Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: Searched: 1825181 seqs, 575374646 residues

1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Ļ | | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 80 | 7 | თ | v, | ٠. | w | Ŋ | ۳ | NO. | Result | |
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| | 347 | 347 | 466 | 374 | 350 | 350 | 359 | 349 | 349 | 349 | 350 | 350 | 350 | 350 | 349 | 457 | 352 | 428 | 428 | 428 | 429 | 429 | 428 | 428 | 428 | 465 | 468 | 491 | 491 | 461 | 457 | rengen | | |
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ALIGNMENTS

| g dd | Db Qy | Оу | Oy Db | g Q | Query M Best Lo Matches | ACCOMPANY | RESULT Q48902 |
|---|---|---|--|---|---|--|------------------|
| 232 DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGV 289 : : : : | 172 AGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITT 231 :: : : : : : : : : : : | 120 AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWL 171 :: :: :: :: | 65 SFNQSGWEAIQQLGALTG-GEITSVDSSTAELEGKYKSSLANTNKNVWVLSGFQHGD 119 | 5 ETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN 64 | Query Match 32.2%; Score 693.5; DB 2; Length 457; Best Local Similarity 39.0%; Pred. No. 4.3e-35; Matches 168; Conservative 81; Mismatches 141; Indels 41; Gaps 14; | Q48902 PRELIMINARY; PRT; 457 AA. Q48902 Q18902 PRELIMINARY; PRT; 457 AA. Q48902 Q1. Q49002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q40002 Q1. Q400 | |

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Complete proteome; Lipoprotein.
SEQUENCE 461 AA; 51096 MW;
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GO; GO:0008289; F:lipid binding; IEA.
InterPro; IPR003760; Bmp.
InterPro; IPR008107; Mycoplasma_p48.
InterPro; IPR011050; Pectin_lyas_like.
Pram; PF02668; Bmp; 1.
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MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Se
Moszer I., Dybvig K., Wroblewski H., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
OrderedLocusNameseMYPU_3460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445564; CAC13519.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma pulmonis. - Bacteria; Firmicutes; Myloplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; B90555; B90555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346
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                                                              KKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII---ANQ
                                                                                                                      EAGWQAGYASADFLGTKYANNEAKRAISAFGGGDFAGVTDFLNGFFEGIRAWNSEAENAN
                                                                                                                                                                                                      TTWILTGFQQGNEIENFLNDENNLRRFKENKVKIIGVDWAPNANSKIPQGSLISLLFKTE
                                                                                                                                                                                                                                           NVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIILLGIDWTDTEN-VIPTGRYINLTYKTE 166
                                                                                                                                                                                                                                                                                                                                                                         AQNPNKTNSNLDSSKITDLLSQKEVTETQKIVENKIKQASLETQK-----VVLITADGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM---P
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NDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYT---
                                                                                                                                                             EAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWN--LKNSD
                                                                                                                                                                                                                                                                                                                                                                                                                  ADNONKQIT--DVSKISGLVNER-----KSEIMAAKADANKHFGLNMAIVTAGGTV
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                                         KKVKIVSENLVLDTGF-IPNAEKNEVVSNVVETGKSTISLPVAGPFTGVVVDVLRKDTSD
                                                                                                                                                                                                                                                                                         DDKSFNQQVYESQKTLKDFVDKAYKSQNKEAENQHKLDNYINSAVKDLEQNYKVALDRGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%; Score 552; DB 2
31.2%; Pred. No. 3e-26;
tive 82; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6724D4D820809CE4 CRC64;
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Q6KIQ4;
Q6KIQ4;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Unspecified sugar ABC transporter binding protein.
OrderedLocusNames=MMOB0360;
Mycoplasma mobile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren B.W., Stange-Thomann N., Smith C., DeCaprio D., Fis Butler J., Calvo S., Elkin T., FitzGerald M.G., Hafez N., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AE017337; AAT27522.1; InterPro; IPR008107; Mycoplasma_p48.

PRINTS; PR01733; LIPPROTEIN48.
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STRAIN=163K / ATCC 43663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                             381
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LAASLALFNKNKAKIIATIP------VQIPNFSGGPSTPEQIPNPLNELIKKIN
                                          ------BEKTK---TIPAEEVRKTLEIPEMP--DKQPDKQQESLDKLITDIN
                                                                                 SSLP-----LANADITKGFVESTEPVDFVGFSKSALGGKITQSLVQANVGRSFAEVADEY
                                                                                                                                                                     AKAFSPDLAKLFFSSVEKNVAGTTYAALASLYLGTVSTDPFFNITGSSSRFIPVTEKNNS
                                                                                                                                                                                                             SLVYTKTKNK-FFTSILKNLGYSVFSVLSDLY-----TKKSNS
                                                                                                                                                                                                                                                      NTGFAV----TPEAATAIQSIVGSGTQVVFPVAGSLTTLTVNSISQENSGQFVIGVDSDQ
                                                                                                                                                                                                                                                                                             NLGFDVQDTSTKERLEQIASKDKPST--LLAVAGPLTEIFSDIIANQND-RYLIGVDTDQ
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR903610, AAB99740.1;
GO; GO:0008289; F:lipid binding; IEA.
InterPro; IPR003760; Bmp.
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
PRINTS; PR01733; LIPPROTEIN48.
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O52311;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein; Signal.
SIGNAL 1
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                          NERKSEIMAAKADANKH----
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27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EIQKSLK
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                                                                        86;
                                                                        Score 384.5; DB 2;
Pred. No. 7.8e-16;
86; Mismatches 157;
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60AD5448CFE03C96 CRC64;
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Matches 116
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=9911554; PubMed=9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S. "Differential posttranslational processing confers intraspeci variation of a major surface lipoprotein and a macrophage-act lipopeptide of Mycoplasma fermentans."; Infect. Immun. 67:760-771(1999).
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NCBI_TaxID=2115;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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SIGNAL 1
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                                                                                                                                                                                          116;
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                              75
                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKIT-TDKIEINLGFDVQDTSTKERLEQ
QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVMVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
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                                                                                                                                     NERKSEIMAAKADANKH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLEATISAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDKLITDIN 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ-----KEKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VINNVLSSTPADVKYNPHVILSVAGPAT -- FETVKLANKGQYVIGVDSDQGMI -- QDKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAINKQTGIEINSVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
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                                                                                   NNDESNÍSFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNOSAFEAL
                                                                                                                                                                                                                                                                                           1 24 Potential.
25 428 macrophage activating lipoprotein-404
428 AA; 47835 MW; D03F0F47EA2B1460 CRC64;
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                           17.7%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma_p48
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                                                                                                                                                                                          87;
                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                   Score 382.5; DB 2; Pred. No. 1e-15;
                                                                                                                                                                                          Mismatches
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                                                                                                                                     ----FGLNMAIVTAGGTVNDNSFNQSGWEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ng confers intraspecies
and a macrophage-activating
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                                                                                                                                                                                             156;
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Best Local S
Matches 141
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Unspecified
MMOB0360.
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AAT27522;
24-MAY-2004
24-MAY-2004
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Jaffe J.D., Church G.M.;
Jaffe J.D., Church G.M.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ
EMBL; AE017337; AAT27522.1; -.
CTOTITUDE 491 AA; 52817 MW; 2D1C707687771B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren B.W., Stange-Thomann N., Smith C., DeCaprio D., Fis Butler J., Calvo S., Elkin T., FitzGerald M.G., Hafez N., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma mobile 163K.
Bacteria; Firmicutes; M
Wycoplasma mobile.
MYCOI TaxID=267748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berg H.C.;
Submitted (APR-2004)
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                                                                           RNLAGFEFGKKSATVYLGIKDR-----FVDIADTSLEGNDKKLATEA----ISEAKKEF
                                                                                                                             SLVYTKTKNK-FFTSILKNLGYSVFSVLSDLY------
                                                                                                                                                                                NLGFDVQDTSTKERLEQIASKDKPST--LLAVAGPLTEIFSDIIANQND-RYLIGVDTDQ
                                                                                                                                                                                                        -RTFNTFGGGAFPEVTNFNAGFLQGILDFN--NSTFLEPGETSITDNKKLSFTPGDIINI
                                                                                                                                                                                                                       NKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPT
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                                                   SSLP-----LANADITKGFVESTEPVDFVGFSKSALGGKITQSLVQANVGRSFAEVADEY
                                                                                                    AKAFSPDLAKLFFSSVEKNVAGTTYAALASLYLGTVSTDPFFNITGSSSRFIPVTEKNNS
                                                                                                                                                                                                                                                           NRAEFIRKQVIIVAIDWTTNLELVPPGQFISINYRTQESSWIVGNAVAKFISDNHNNN--
                                                                                                                                                                                                                                                                                                                                     QQLGALTG--GEITSVDSSTA---ELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPE
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
sugar ABC transporter binding protein.
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                        EEKTK---TIPAEEVRKTLEIPEMP--DKQPDKQQESLDKLITDIN
                                                                                                                                                      -TPEAATAIQSIVGSGTQVVFPVAGSLTTLTVNSISQENSGQFVIGVDSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                21.6%; Score 465.5; DB 2
29.7%; Pred. No. 8.2e-21;
tive 80; Mismatches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      င်
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2D1C707687771B41
- VQIPNFSGGPSTPEQIPNPLNELIKKIN
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Q6E5B5;
01-OCT-2004 (TrEMBLrel.:
01-OCT-2004 (TrEMBLrel.:
01-OCT-2004 (TrEMBLrel.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9X775;
Q9X775;
01-NOV-1999
"P48 major surface antigen of Mycoplasma a malp product of Mycoplasma fermentans and of bacterial lipoproteins."; Infect. Immun. 67:6213-6216 (1999).
EMBL; AJ132423; CAB43718.1; -.
GO; GO:0008289; F:lipid binding; IEA.
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Rosati S., Alberti A., Robino P., Pittau M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AY557344; AAT64137.1; -.
SEQUENCE 468 AA; 51175 MW; AA0333F810ED2FFE CRC64;
                                                                                                                                                                                             MEDLINE=20002620;
Rosati S., Pozzi S
Pittau M.;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma agalactiae Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=p48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P48 membrane lipoprotein
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01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIANKALEEATKYYESK-----KAEIQKTLSGQLEEAKKALGTKWPDQPADQFGKMI
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S., Robino P., Montinaro
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Last annotation updat
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Pred. No. 1.2e-17;
7; Mismatches 140
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Query Match
Best Local Similarity
Matches 115; Conserv
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032417;
01-JAN-1998
01-JAN-1998
05-JUL-2004
                                                                                 GO; GO:0000200760; Bmp.
InterPro; IPR003760; Bmp.
InterPro; IPR008107; Mycoplasma_p48.
Pfam; PF02608; Bmp; 1.
PRINTS; PR01733; LIPPROTEIN48.
PRINTS; PR01733; LIPPROTEIN48.
                                                                                                                                                                                                                      Seya T., Matsumoto M.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ
EMBL; D64083; BAA23530.1; -.
EMBL; AB026157; BAA77211.2; -.
GO; GO:0008289; F:lipid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                    M161Ag, a Mycoplasma fermentans gene product production by human monocytes.";
J. Biol. Chem. 273:12407-12414(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98241611; PubMed=9575196;
Matsumoto M., Nishiguchi M., Kikkawa S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone marrow;
MEDILINE=98022661; PubMed=9359703;
Matsumoto M., Takeda J., Inoue N., Hara T., Hatanaka M., Taka
Nagasawa S., Akedo H., Seya T.;
"A novel protein that participates in nonself discrimination
malignant cells by homologous complement.";
Nat. Med. 3:1266-1270(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seya T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAINKQTGIEINSVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
       17.6%; Score 379.5; DB 2; 26.7%; Pred. No. 1.6e-15; ive 88; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mollicutes; Mycoplasmataceae; Mycoplasma
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Last sequence update)
Last annotation updat
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                                                                                                        F43B078F21DADD6E CRC64;
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          71;
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          17;
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Q9RGX4
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Matches
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Lipoprotein; Signal.
SIGNAL 1
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01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-MAR-2004 (TrEMBLrel 26, Last annotation updat
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                            InterPro; IPR003760; Bmp.
InterPro; IPR008107; Mycoplasma_p48
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma fermentans. Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2115;
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                                                                                                                                  Local
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                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
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            NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
                                                        NERKSEIMAAKADANKH-------FGLNMAIVTAGGTVNDNSFNOSGWEAI
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429 AA;
                                                                                                        17.6%;
larity 26.9%;
Conservative 8
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                                                                                                                                                                                                  Potential.
macrophage activating lipoprotein-404
NW; B6D08CF975AC3171 CRC64;
                                                                                                           ; 68
                                                                                                        Score 379; DB 2;
Pred. No. 1.7e-15;
9; Mismatches 154;
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Best Local
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MEDLINE=9911554; PubMed=9916088;

Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;

"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activa lipopeptide of Mycoplasma fermentans.";

Infect. Immun. 67:760-771(1999).

EMBL; AF099210; AAD16394.1; ---

GO; GO:0008289; F:lipid binding; IEA.
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Q9RGX6;
01-MAY-2000
01-MAY-2000
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein; Signal.
SIGNAL 1
CHAIN 25 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update
01-MAR-2004 (TrEMBLrel. 26, Last annotation upda
Macrophage activating lipoprotein-404 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008107; Mycoplasma_p48 Pfam; PF02608; Bmp; 1. PRINTS; PR01733; LIPPROTEIN48.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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                                                                                                                                                                                                                                                                   Similarity
KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                             NERKSEIMAAKADANKH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESLDKLITDIN 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLAANKGQYVIGVDSDQGMI--QDKD
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                                                        QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF
                                                                                                                 NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
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                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                 429 macrophage activating lip
47961 MW; B6D09A8812AC3171 CRC64;
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                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                             Score 379; DB 2;
Pred. No. 1.7e-15;
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-9911554; PubMed-9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; "Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-active lipopsptide of Mycoplasma fermentans."; Immun. 67:760-771(1999).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PRINTS; PR01733; LIPPROTEIN48.
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InterPro; IPR008107; Mycoplasma_p48.
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                                                        WLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI
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  FTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKI
                                                                                                                    WVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AA;
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                 Score 377.5; DB 2;
Pred. No. 2.1e-15;
4; Mismatches 146;
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Best Local Similarity
Matches 115; Conserv
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Q9RGX3;
01-MAY-2000
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SIGNAL 1
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GO; GO:0008289; F:lipid binding; IEA.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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PRINTS; PR01733; LIPPROTEIN48.
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InterPro; IPR008107; Mycoplasma_p48.
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                                VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                          IAS------KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
                                                                                                                                                                                                                                                        ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKEPAFTTGYAIASWLSEQ---DESKRVVA
                                                                                                                                                                                                                                                                                                          TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
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                                                                                                                                                                                              VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 253
                                                                                                                                                                                                                                                                                                                                                                     KAINKQTGIEINSVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEDFVKYINSDKALKDGNKIDNVSERLEAIISAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 r
47875 MW;
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Pred. No. 3.3e-1
6; Mismatches 1
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macrophage activating lipoprotein-404.
; C7A536B409A60132 CRC64;
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3e-15;
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Best Local
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SEQUENCE
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MEDLINE=99115554; PubMed=9916088;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt
"Differential posttranslational processing co
variation of a major surface lipoprotein and
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein; Signal.
SIGNAL 1
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02608; Bmp; PRINTS; PR01733; LII
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EMBL; AF099214; AAD16398.1; -.
EMBL; AF099215; AAD16399.1; -.
GO; GO:0008289; F:lipid binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mycoplasma fermentans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor).
Name=malP;
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InterPro; IPR008107; Mycoplasma_p48.
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115; Conserv
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                                                          VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
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     FFTSILKNLGYSVFSVLSDL---
                                                                                                                                                                         SFGVGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                                                                                                                                                                                                              VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 253
                                                                                                                                                                                                                                                                                      ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA
                                                                                                                                                                                                                                                                                                                                        TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                                                                                                                                                                                     KAINKQTGIEINSVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQLGALTGGETTSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF
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428 AA;
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38 m
47863 MW;
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26.7%;
                                                                                                               KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 373.5; DB 2;
Pred. No. 3.8e-15;
7; Mismatches 157;
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; 59808324E218F03C CRC64;
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Muhlradt

P.F.,

Wise K.S

Mycoplasma

lipoprotein-404

a macrophage-activating

DB 2;

Length Indels

428; 71;

Gaps

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143

134 98

197

MALP-2.

-YTKKSNSRNLAGFEFGKKSATVYLGIKDRF

353 306 250

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A Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Y.
A Chen Y., Xue Y., Li X., Huang L., Dong X., Ma Y.,
A Tan H., Chen R., Wang J., Yu J., Yang H.;
T "A complete sequence of the T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
R EMBL; AE013017; AAM23740.1; -.
R GO; GO:0008289; F:lipid binding; IEA.
InterPro; IPR003760; Bmp.
R Ffam; PF02608; Bmp; D.
Complete protecome; Lipoprotein.
SEQUENCE 352 AA; 38052 MW; DCA7990EA271A23B CRC64;
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Best Local Similarity
Matches 94; Conserv
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Q8RCH2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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Name=Med; OrderedLocusNames=TTE0457;
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                                                        365
348
                                                                                                                    292
                                                                                                                                                                          319 VLSD------LYTKKSNSRNLAGFEFGKKSATVYLGIKDRF----VDIADTSLEGN 364
                                                                                                                                                                                                                                     238 EIIFQVAGGTGE---GVIKAAQEKNLYAIGVDADQSYL---APDNVLTSAVKRVDVAVYD 291
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DK 349
                                                           DK 366
                                                                                                              VIKDALNGNFKSGIMYFDLKNN----GVGLGKINKDVPQSIIDQVNQLAKDIIDGKIQVS 347
                                                                                                                                                                                                                                                                        STLLAVAGPLTEIFSDII--ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFS 318
                                                                                                                                                                                                                                                                                                                                                          IPPVDRFIAGYQQGAKAVN------PDIKILINYTNNFNDPAAGKQMALTQISQGA 237
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X., Ma Y., Ling
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Search completed: December 18, 2004, 01:26:33 Job time : 121.543 secs